

# SEQUENCE LISTING

<110> Odyssey Thera, Inc.  
 Michnick, Stephen  
 MacDonald, Marnie  
 Lamerdin, Jane

<120> FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT  
 COMPLEMENTATION ASSAYS

<130> ODDY007

<150> US 60/461,133

<151> 2003-04-09

<160> 1067

<170> PatentIn version 3.0

<210> 1

<211> 714

<212> DNA

<213> Aequorea victoria

<220>

<221> CDS

<222> (1)..(714)

<223> wild-type green fluorescent protein

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gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg aaa cgg	240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	

aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat gga	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aaa gtt aac ttc aaa att aga cac aac att gaa gat gga agc gtt	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct	576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	
180 185 190	
gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcg	624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser	
195 200 205	
aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta	672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val	
210 215 220	
aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa	714
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys	
225 230 235	

<210> 2  
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 <212> PRT  
 <213> Aequorea victoria

<400> 2

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20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
225 230 235

<210> 3  
<211> 239  
<212> PRT  
<213> Artificial

<220>  
<223> "EGFP", an Aequorea-derived mutated variant of wild-type green fl  
uorescent protei

<300>  
<301> Zhang, J. et al  
<302> Creating new fluorescent probes for cell biology  
<303> Nat. Rev. Mol. Cell Biol.  
<304> 3  
<305> 12  
<306> 906-918  
<307> 2002-\_\_ -\_\_  
<313> (1)..(239)

<400> 3

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125  
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140  
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
145 150 155 160  
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175  
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190  
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
195 200 205  
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210  
215 220  
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
225 230 235

<210> 4

<211> 239

<212> PRT

<213> Artificial

<220>

<223> "EYFP", enhanced yellow fluorescent protein, an Aequorea-derived  
mutated variant of wild-type green fluorescent protei

<300>

<301> Zhang, J. et al

<302> Creating new fluorescent probes for cell biology

<303> Nat. Rev. Mol. Cell Biol.



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<220>
<223>  "EYFP-Q69M", citrine fluorescent protein variant of EYFP, a Met
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residue replaces Gln at position 69 (numbering is relative to wt GFP)

<300>

<301> Zhang, J. et al.

<302> Creating new fluorescent probes for cell biology

<303> Nat. Rev. Mol. Cell Biol.

<304> 3

<305> 12

<306> 906-918

<307> 2002-\_\_-\_\_

<313> (1)..(239)

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
          20          25          30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
          35          40          45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
          50          55          60

Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65          70          75          80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
          85          90          95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
          100          105          110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
          115          120          125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
          130          135          140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145          150          155          160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
          165          170          175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
          180          185          190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
          195          200          205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
          210          215          220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225          230          235

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<210> 6  
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 <223> "SEYFP", super enhanced yellow fluorescent protein, a mutated variant of EYF  
  
 <300>  
 <301> Zhang, J. et al  
 <302> Creating new fluorescent probes for cell biology  
 <303> Nat. REv. Mol. Cell Biol.  
 <304> 3  
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 <306> 906-918  
 <307> 2002-\_\_-\_\_  
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 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
  
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
  
 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly  
 165 170 175  
  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu  
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

<210> 7  
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 <212> PRT  
 <213> Artificial

<220>  
 <223> "SEYFP-F46L" known as 'Venus' fluorescent protein, a mutated variant of SEYFP; " Leu" replaces" Phe" at position 46 (numbering is relative to wt GFP

<300>  
 <301> Zhang, J. et al  
 <302> Creating new fluorescent probes for cell biology  
 <303> Nat. Rev. Mol. Cell Biol.  
 <304> 3  
 <305> 12  
 <306> 906-918  
 <307> 2002-\_\_\_\_\_  
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn  
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly  
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu  
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
225 230 235

<210> 8

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<213> Artificial

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<223> "ECFP", cyan fluorescent protein, an Aequorea-derived mutated variant of wt green fluorescent protein

<300>

<301> Zhang, J. et al

<302> Creating new fluorescent probes for cell biology

<303> Nat. Rev. Mol. Cell Biol.

<304> 3

<305> 12

<306> 906-918

<307> 2002- -

<313> (1)..(239)

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn  
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
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<210> 9  
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<213> Anthozoa zoanthus;

<220>  
<221> misc\_feature  
<223> Zoanthus ("z") FP506

<300>  
<301> Matz, M.V. et al  
<302> Fluorescent proteins from nonbioluminescent Anthozoa species  
<303> Nat. Biotech.  
<304> 17  
<305> 10  
<306> 969-73  
<307> 1999-\_\_\_\_\_  
<313> (1)..(231)

<400> 9

Met Ala Gln Ser Lys His Gly Leu Thr Lys Phe Met Thr Met Lys Tyr  
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Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile Thr Gly Glu  
20 25 30

Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Ala Ile Asn Leu Cys Val  
35 40 45

Val Glu Gly Gly Pro Leu Pro Phe Ala Glu Asp Ile Leu Ser Ala Ala  
50 55 60

Phe Asn Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln Asp Ile Val  
65 70 75 80

Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Asp Arg Ser  
85 90 95

Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala Asp Ile Thr  
100 105 110

Val Ser Val Glu Glu Asn Cys Met Tyr His Glu Ser Lys Phe Tyr Gly  
115 120 125

Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Asp Asn

130

135

140



Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Val Pro Lys Gln Gly Ile  
145 150 155 160

Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Lys Asp Gly Gly Arg  
165 170 175

Leu Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Arg  
180 185 190

Lys Met Pro Asp Trp His Phe Ile Gln His Lys Leu Thr Arg Glu Asp  
195 200 205

Arg Ser Asp Ala Lys Asn Gln Lys Trp His Leu Thr Glu His Ala Ile  
210 215 220

Ala Ser Gly Ser Ala Leu Pro  
225 230

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<213> Anthozoa zoanthus;

<220>

<221> misc\_feature

<223> Zoanthus ("z") FP538

<300>

<301> Matz, M.V. et al

<302> Fluorescent proteins from nonbioluminescent Anthozoa species

<303> Nat. Biotech.

<304> 17

<305> 10

<306> 969-73

<307> 1999-\_\_-\_\_

<313> (1)..(231)

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His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu  
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Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val  
35 40 45

Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly  
50 55 60

Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val  
65 70 75 80

Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Arg Ser  
85 90 95

Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr

100										105					110				
Val	Ser	Val	Lys	Glu	Asn	Cys	Ile	Tyr	His	Lys	Ser	Ile	Phe	Asn	Gly				
		115					120					125							
Met	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Met	Thr	Thr	Asn				
	130					135					140								
Trp	Glu	Ala	Ser	Cys	Glu	Lys	Ile	Met	Pro	Val	Pro	Lys	Gln	Gly	Ile				
145					150					155					160				
Leu	Lys	Gly	Asp	Val	Ser	Met	Tyr	Leu	Leu	Leu	Lys	Asp	Gly	Gly	Arg				
			165					170						175					
Tyr	Arg	Cys	Gln	Phe	Asp	Thr	Val	Tyr	Lys	Ala	Lys	Ser	Val	Pro	Ser				
			180					185					190						
Lys	Met	Pro	Glu	Trp	His	Phe	Ile	Gln	His	Lys	Leu	Leu	Arg	Glu	Asp				
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Arg	Ser	Asp	Ala	Lys	Asn	Gln	Lys	Trp	Gln	Leu	Thr	Glu	His	Ala	Ile				
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Ala	Phe	Pro	Ser	Ala	Leu	Ala													
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<213> Anthozoa discosoma;

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<221> misc\_feature

<223> Discosoma striata ("ds") FP483

<300>

<301> Matz, M.V. et al

<302> Fluorescent proteins from nonbioluminescent Anthozoa species

<303> Nat. Biotech.

<304> 17

<305> 10

<306> 969-73

<307> 1999-\_\_-\_\_

<313> (1)..(232)

<400> 11

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His	Leu	Glu	Gly	Thr	Phe	Asn	Gly	His	Tyr	Phe	Phe	Ile	Lys	Gly	Lys
			20					25					30		
Gly	Lys	Gly	Gln	Pro	Asn	Glu	Gly	Thr	Asn	Thr	Val	Thr	Leu	Glu	Val
		35					40					45			
Thr	Lys	Gly	Gly	Pro	Leu	Pro	Phe	Gly	Trp	His	Ile	Leu	Cys	Pro	Gln
	50					55					60				

Phe Gln Tyr Gly Asn Lys Ala Phe Val His His Pro Asp Asn Ile His  
 65 70 75 80  
 Asp Tyr Leu Lys Leu Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser  
 85 90 95  
 Met His Phe Glu Asp Gly Gly Leu Cys Cys Ile Thr Asn Asp Ile Ser  
 100 105 110  
 Leu Thr Gly Asn Cys Phe Tyr Tyr Asp Ile Lys Phe Thr Gly Leu Asn  
 115 120 125  
 Phe Pro Pro Asn Gly Pro Val Val Gln Lys Lys Thr Thr Gly Trp Glu  
 130 135 140  
 Pro Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Ile Gly Asp  
 145 150 155 160  
 Ile His His Ala Leu Thr Val Glu Gly Gly Gly His Tyr Ala Cys Asp  
 165 170 175  
 Ile Lys Thr Val Tyr Arg Ala Lys Lys Ala Ala Leu Lys Met Pro Gly  
 180 185 190  
 Tyr His Tyr Val Asp Thr Lys Leu Val Ile Trp Asn Asn Asp Lys Glu  
 195 200 205  
 Phe Met Lys Val Glu Glu His Glu Ile Ala Val Ala Arg His His Pro  
 210 215 220  
 Phe Tyr Glu Pro Lys Lys Asp Lys  
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<210> 12

<211> 226

<212> PRT

<213> Anthozoa discosoma;

<220>

<221> misc\_feature

<223> Discosoma red ("dr") FP583

<300>

<301> Matz, M.V. et al

<302> Fluorescent proteins from nonbioluminescent Anthozoa species

<303> Nat. Biotech.

<304> 17

<305> 10

<306> 969-73

<307> 1999-\_\_-\_\_

<313> (1)..(226)

<400> 12

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val  
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Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Phe Ile Glu Gly Glu  
 20 25 30

Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val  
 35 40 45  
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln  
 50 55 60  
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro  
 65 70 75 80  
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val  
 85 90 95  
 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser  
 100 105 110  
 Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn  
 115 120 125  
 Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu  
 130 135 140  
 Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu  
 145 150 155 160  
 Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu  
 165 170 175  
 Phe Lys Ser Ile Tyr Met Ala Lys Lys Ala Pro Val Gln Leu Pro Gly  
 180 185 190  
 Tyr Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp  
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 Tyr Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu  
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Phe Leu  
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 <213> Anthozoa anemonia majano;

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 <223> anemonia majano ("am") FP486

<300>  
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 <302> Fluorescent proteins from nonbioluminescent Anthozoa species  
 <303> Nat. Biotech.  
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 <307> 1999-\_\_-\_\_  
 <313> (1)..(229)

<400> 13

Met Ala Leu Ser Asn Lys Phe Ile Gly Asp Asp Met Lys Met Thr Tyr  
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His Met Asp Gly Cys Val Asn Gly His Tyr Phe Thr Val Lys Gly Glu  
20 25 30

Gly Asn Gly Lys Pro Tyr Glu Gly Thr Gln Thr Ser Thr Phe Lys Val  
35 40 45

Thr Met Ala Asn Gly Gly Pro Leu Ala Phe Ser Phe Asp Ile Leu Ser  
50 55 60

Thr Val Phe Lys Tyr Gly Asn Arg Cys Phe Thr Ala Tyr Pro Thr Ser  
65 70 75 80

Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu  
85 90 95

Arg Thr Phe Thr Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Glu  
100 105 110

Ile Ser Leu Lys Gly Asn Cys Phe Glu His Lys Ser Thr Phe His Gly  
115 120 125

Val Asn Phe Pro Ala Asp Gly Pro Val Met Ala Lys Lys Thr Thr Gly  
130 135 140

Trp Asp Pro Ser Phe Glu Lys Met Thr Val Cys Asp Gly Ile Leu Lys  
145 150 155 160

Gly Asp Val Thr Ala Phe Leu Met Leu Gln Gly Gly Gly Asn Tyr Arg  
165 170 175

Cys Gln Phe His Thr Ser Tyr Lys Thr Lys Lys Pro Val Thr Met Pro  
180 185 190

Pro Asn His Val Val Glu His Arg Ile Ala Arg Thr Asp Leu Asp Lys  
195 200 205

Gly Gly Asn Ser Val Gln Leu Thr Glu His Ala Val Ala His Ile Thr  
210 215 220

Ser Val Val Pro Phe  
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<210> 14

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<212> PRT

<213> Anthozoa clavularia;

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<221> misc\_feature

<223> Clavularia ("c") FP484

<300>

<301> Matz, M.V. et al

<302> Fluorescent proteins from nonbioluminescent Anthozoa species

<303> Nat. Biotech.

<304> 17

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<306> 969-73

<307> 1999- -

<313> (1)..(231)

<400> 14

Lys Ala Leu Thr Thr Met Gly Val Ile Lys Pro Asp Met Lys Ile Lys  
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Leu Lys Met Glu Gly Asn Val Asn Gly His Ala Phe Val Ile Glu Gly  
20 25 30

Glu Gly Glu Gly Lys Pro Tyr Asp Gly Thr His Thr Leu Asn Leu Glu  
35 40 45

Val Lys Met Ala Glu Gly Ala Pro Leu Pro Phe Ser Tyr Asp Ile Leu  
50 55 60

Ser Asn Ala Phe Gln Tyr Gly Asn Arg Ala Leu Thr Lys Tyr Pro Asp  
65 70 75 80

Asp Ile Ala Asp Tyr Phe Lys Gln Ser Phe Pro Glu Gly Tyr Ser Trp  
85 90 95

Glu Arg Thr Met Thr Phe Glu Asp Lys Gly Ile Val Lys Val Lys Ser  
100 105 110

Asp Ile Ser Met Glu Glu Asp Ser Phe Ile Tyr Glu Ile Arg Phe Asp  
115 120 125

Gly Met Asn Phe Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Leu  
130 135 140

Lys Trp Glu Pro Ser Thr Glu Ile Met Tyr Val Arg Asp Gly Val Leu  
145 150 155 160

Val Gly Asp Ile Ser His Ser Leu Leu Leu Glu Gly Gly Gly His Tyr  
165 170 175

Arg Cys Asp Phe Lys Ser Ile Tyr Lys Ala Lys Lys Val Val Lys Leu  
180 185 190

Pro Asp Tyr His Phe Val Asp His Arg Ile Glu Ile Leu Asn His Asp  
195 200 205

Lys Asp Tyr Asn Lys Val Thr Leu Tyr Glu Asn Ala Val Ala Arg Tyr  
210 215 220

Ser Leu Leu Pro Ser Gln Ala  
225 230

<210> 15

<211> 675

<212> DNA

<213> Artificial

<220>

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<223>  "mRFP1", an engineered monomeric form of DsRed  FP

<220>
<221>  CDS
<222>  (1)..(675)

<300>
<301>  Campbell, R.E. et al
<302>  A monomeric red fluorescent protein
<303>  Proc. Nat'l. Acad. Sci.
<304>  99
<305>  12
<306>  7877-82
<307>  2002-06-11
<313>  (1)..(675)

<400>  15
atg gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg      48
Met Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val
1          5          10          15

cgc atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag      96
Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
          20          25          30

ggc gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg      144
Gly Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val
          35          40          45

acc aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag      192
Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
          50          55          60

ttc cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc      240
Phe Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro
65          70          75          80

gac tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg      288
Asp Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
          85          90          95

atg aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc      336
Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
          100          105          110

ctg cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac      384
Leu Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn
          115          120          125

ttc ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag      432
Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
          130          135          140

gcc tcc acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag      480
Ala Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu
145          150          155          160

atc aag atg agg ctg aag ctg aag gac ggc ggc cac tac gac gcc gag      528
Ile Lys Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu
          165          170          175

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gtc aag acc acc tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc  
Val Lys Thr Thr Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala  
180 185 190

576



tac aag acc gac atc aag ctg gac atc acc tcc cac aac gag gac tac	624
Tyr Lys Thr Asp Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr	
195 200 205	

acc atc gtg gaa cag tac gag cgc gcc gag ggc cgc cac tcc acc ggc	672
Thr Ile Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly	
210 215 220	

gcc	675
Ala	
225	

<210> 16  
 <211> 225  
 <212> PRT  
 <213> Artificial

<220>  
 <223> "mRFP1", an engineered monomeric form of DsRed FP

<400> 16

Met Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val
1 5 10 15

Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
20 25 30

Gly Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val
35 40 45

Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
50 55 60

Phe Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro
65 70 75 80

Asp Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
85 90 95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
100 105 110

Leu Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn
115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
130 135 140

Ala Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu  
145 150 155 160

Ile Lys Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu  
165 170 175

Val Lys Thr Thr Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala  
180 185 190

Tyr Lys Thr Asp Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr  
195 200 205

Thr Ile Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly  
210 215 220

Ala  
225

<210> 17  
<211> 696  
<212> DNA  
<213> Artificial

<220>  
<223> "KFP1" a mutated variant of kindling fluorescent protein asCP from *A. sulcata*

<220>  
<221> CDS  
<222> (1)..(696)

<400> 17  
atg gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag 48  
Met Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu  
1 5 10 15  
ggc acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc 96  
Gly Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly  
20 25 30  
aac ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc 144  
Asn Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly  
35 40 45  
ggc ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac 192  
Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr  
50 55 60  
ggc tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc 240  
Gly Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe  
65 70 75 80

aag cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac	288
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr	
85 90 95	
 gag gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc	336
Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly	
100 105 110	
 gac tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc	384
Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala	
115 120 125	
 gac ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc	432
Asp Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr	
130 135 140	
 gag atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg	480
Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met	
145 150 155 160	
 gcc ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc	528
Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr	
165 170 175	
 acc tac cgc tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc ttc	576
Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe	
180 185 190	
 cac ttc gag gac cac cgc atc gag atc atg gag gag gtg gag aag ggc	624
His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly	
195 200 205	
 aag tgc tac aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac gcc	672
Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala	
210 215 220	
 gcc ccc tcc aag ctg ggc cac aac	696
Ala Pro Ser Lys Leu Gly His Asn	
225 230	

<210> 18

<211> 232

<212> PRT

<213> Artificial

<220>

<223> "KFP1" a mutated variant of kindling fluorescent protein asCP from *A. sulcata*

<400> 18

Met Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu
1 5 10 15

Gly Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly
20 25 30

Asn Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly  
 35 40 45

Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr  
 50 55 60

Gly Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe  
 65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr  
 85 90 95

Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly  
 100 105 110

Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala  
 115 120 125

Asp Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr  
 130 135 140

Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met  
 145 150 155 160

Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr  
 165 170 175

Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe  
 180 185 190

His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly  
 195 200 205

Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala  
 210 215 220

Ala Pro Ser Lys Leu Gly His Asn  
 225 230

<210> 19  
 <211> 10  
 <212> PRT  
 <213> Artificial

<220>  
 <223> flexible linker

<400> 19

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10

<210> 20

<211> 114

<212> DNA

<213> Artificial

<220>

<223> modified fragment= GFP F1(aa 1-39 of wt GFP) w/o. Met @ position  
1

<220>

<221> CDS

<222> (1)..(114)

<400> 20

agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att ctt gtt gaa 48  
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu  
1 5 10 15

tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag ggt 96  
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly  
20 25 30

gaa ggt gat gca aca tac 114  
Glu Gly Asp Ala Thr Tyr  
35

<210> 21

<211> 38

<212> PRT

<213> Artificial

220>

<223> modified fragment= GFP F1 (aa 1-39 of wt GFP) w/o. Met @ position  
1

<400> 21

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu  
1 5 10 15

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly  
20 25 30

Glu Gly Asp Ala Thr Tyr  
35

<210> 22

<211> 600

<212> DNA

<213> Artificial

<220>  
 <223> modified frag.; GFP F2 (aa 40-238 of wt GFP) + Met @ position 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 22

atg gga aaa ctt acc ctt aaa ttt att tgc act act gga aaa cta cct	48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
1 5 10 15	
ggt cca tgg cca aca ctt gtc act act ttc tct tat ggt gtt caa tgc	96
Val Pro Trp Pro Thr Leu Val Thr Phe Ser Tyr Gly Val Gln Cys	
20 25 30	
ttt tca aga tac cca gat cat atg aaa cgg cat gac ttt ttc aag agt	144
Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
gcc atg ccc gaa ggt tat gta cag gaa aga act ata ttt ttc aaa gat	192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
gac ggg aac tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc	240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	
ctt gtt aat aga atc gag tta aaa ggt att gat ttt aaa gaa gat gga	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
aac att ctt gga cac aaa ttg gaa tac aac tat aac tca cac aat gta	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
100 105 110	
tac atc atg gca gac aaa caa aag aat gga atc aaa gtt aac ttc aaa	384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
115 120 125	
att aga cac aac att gaa gat gga agc gtt caa cta gca gac cat tat	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
caa caa aat act cca att ggc gat ggc cct gtc ctt tta cca gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cat tac ctg tcc aca caa tct gcc ctt tcg aaa gat ccc aac gaa aag	528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
aga gac cac atg gtc ctt ctt gag ttt gta aca gct gct ggg att aca	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
cat ggc atg gat gaa cta tac aaa	600
His Gly Met Asp Glu Leu Tyr Lys	

195

200

<210> 23  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>

<223> modified frag.; GFP F2 (aa 40-238 of wt GFP) + Met @ position 1

<400> 23

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys  
 20 25 30

Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190



His Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 24  
 <211> 117  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modified frag.; YFP F1A (aa 1-40 of EYFP) - Met @ position 1

<220>  
 <221> CDS  
 <222> (1)..(117)

<400> 24  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac 117  
 Gly Glu Gly Asp Ala Thr Tyr  
 35

<210> 25  
 <211> 39  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modified frag.; YFP F1A (aa 1-40 of EYFP) - Met @ position 1

<400> 25

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr  
 35

<210> 26  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modified frag.; YFP F2A (aa 41-239 of EYFP) + Met @ position 1

<220>  
 <221> CDS  
 <222> (1)..(600)

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<400> 26
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc      48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1                               5                               10                               15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc      96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
                20                               25                               30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
                35                               40                               45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
                50                               55                               60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                               70                               75                               80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                               90                               95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
                100                               105                               110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
                115                               120                               125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                130                               135                               140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                               150                               155                               160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                               170                               175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
                180                               185                               190

ctc ggc atg gac gag ctg tac aag
Leu Gly Met Asp Glu Leu Tyr Lys
                195                               200

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<210> 27

<211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modified frag.; YFP F2A (aa 41-239 of EYFP) + Met @ position 1  
 <400> 27

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 28  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modified frag.; YFPF2A w. F46L mutation  
 <220>  
 <221> CDS  
 <222> (1)..(597)

<400> 28  
 ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110  
 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125  
 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
 tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175  
 gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu

180 185 190

ggc atg gac gag ctg tac aag  
Gly Met Asp Glu Leu Tyr Lys  
195

<210> 29  
<211> 199  
<212> PRT  
<213> Artificial

<220>  
<223> modified frag.; YFPF2A w. F46L mutation

<400> 29

Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 30  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modified frag., YFPF2A w. F46L mutation + Met @ postion 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 30  
atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80  
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95  
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110  
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125  
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140  
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn

145		150		155		160	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag							528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys							
	165			170		175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act							576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr							
	180		185			190	
ctc ggc atg gac gag ctg tac aag							600
Leu Gly Met Asp Glu Leu Tyr Lys							
	195		200				

<210> 31  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modified frag., YFPF2A w. F46L mutation + Met @ postion 1

<400> 31

Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro															
1			5				10					15			
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys															
			20				25					30			
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser															
	35					40				45					
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp															
	50				55				60						
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr															
65				70				75					80		
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly															
			85				90						95		
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val															
	100						105						110		
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys															
	115					120				125					
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr															
	130				135				140						

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 32

<211> 597

<212> DNA

<213> Artificial

<220>

<223> modified frag.; YFPF2A with F46L/F64L mutations

<220>

<221> CDS

<222> (1)..(597)

<400> 32

ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe  
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile



115	120	125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag			432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac			480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
145	150	155	160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc			528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc			576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu			
180	185	190	
ggc atg gac gag ctg tac aag			597
Gly Met Asp Glu Leu Tyr Lys			
195			

<210> 33  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modified frag.; YFPF2A with F46L/F64L mutations  
 <400> 33

Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val			
1	5	10	15
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe			
20	25	30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala			
35	40	45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
50	55	60	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
65	70	75	80
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
85	90	95	
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
100	105	110	

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 34  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modified frag.; YFPF2A w. F46L/F64L mutations + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 34  
atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80  
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly

85										90					95					
aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	336				
Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val					
			100				105						110							
tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	384				
Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys					
			115				120						125							
atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	432				
Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr					
			130				135						140							
cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	480				
Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn					
			145				150						160							
cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	528				
His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys					
			165						170						175					
cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	576				
Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr					
			180						185						190					
ctc	ggc	atg	gac	gag	ctg	tac	aag									600				
Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys													
			195			200														

<210> 35  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modified frag.; YFPF2A w. F46L/F64L mutations + Met @ posit. 1

<400> 35

Met	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro
1				5					10					15	

Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Gly	Tyr	Gly	Leu	Gln	Cys
			20					25					30		

Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser
	35						40					45			

Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp
	50					55					60				

Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr
65					70					75				80	

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 36  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modified frag.; YFPF2A with F64L mutation

<220>  
<221> CDS  
<222> (1)..(597)

<400> 36  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe  
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192

Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp		
50						55					60						
ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg		240
Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu		
65					70				75						80		
gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac		288
Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn		
				85				90						95			
atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	tat		336
Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr		
			100					105						110			
atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc		384
Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile		
			115				120						125				
cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag		432
Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln		
			130			135						140					
cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac		480
Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His		
145					150					155					160		
tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc		528
Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg		
				165				170						175			
gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc		576
Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu		
			180					185					190				
ggc	atg	gac	gag	ctg	tac	aag											597
Gly	Met	Asp	Glu	Leu	Tyr	Lys											
			195														

<210> 37  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modified frag.; YFPF2A with F64L mutation  
 <400> 37

Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val		
1				5				10						15			
Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe		
			20					25					30				
Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala		
			35				40						45				

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 38  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modified frag.; YFPF2A w. F64L mutation + Met @ position 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 38  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc 96

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys  
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
100 105 110	
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 39

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modified frag.; YFPF2A w. F64L mutation + Met @ position 1

<400> 39

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15



Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys  
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 40  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modified frag.; YFPF2A with K79R mutation

<220>  
<221> CDS  
<222> (1)..(597)

<400> 40  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg cgc cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110  
 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125  
 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
 tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175  
 gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190  
 ggc atg gac gag ctg tac aag 597  
 Gly Met Asp Glu Leu Tyr Lys  
 195  
 <210> 41  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>

<223> modified frag.; YFPF2A with K79R mutation

<400> 41

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
20 25 30

Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 42

<211> 600

<212> DNA

<213> Artificial

<220>

<223> modified frag.; YFPF2A with K79R mutation + Met @ posit. 1

<220>

<221> CDS

<222> (1)..(600)

<400> 42

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
1 5 10 15	
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc	96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
20 25 30	
ttc gcc cgc tac ccc gac cac atg cgc cgg cac gac ttc ttc aag tcc	144
Phe Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser	
35 40 45	
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
100 105 110	
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	

195

200

<210> 43  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>

<223> modified frag.; YFPF2A with K79R mutation + Met @ posit. 1

<400> 43

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 44  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modified frag.; YFPF2A with Y66F mutation

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 44  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ttc ggc ttc ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110  
 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125  
 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
 tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg

	165		170		175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc						576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu						
	180		185		190	
ggc atg gac gag ctg tac aag						597
Gly Met Asp Glu Leu Tyr Lys						
	195					
<210>	45					
<211>	199					
<212>	PRT					
<213>	Artificial					
<220>						
<223>	modified frag.; YFPF2A with Y66F mutation					
<400>	45					
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val						
1	5		10		15	
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys Phe						
	20		25		30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala						
	35		40		45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp						
	50		55		60	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu						
65	70		75		80	
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn						
	85		90		95	
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr						
	100		105		110	
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile						
	115		120		125	
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln						
	130		135		140	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His						
145	150		155		160	

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 46  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modified frag.; YFPF2A with Y66F mutation + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 46  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc ttc ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80  
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95  
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110  
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125  
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr





cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
                   165                                  170                                  175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
                   180                                  185                                  190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
                   195                                  200

<210> 47  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modified frag.; YFPF2A with Y66F mutation + Met @ posit. 1

<400> 47

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1                                  5                                  10                                  15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys  
                   20                                  25                                  30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
                   35                                  40                                  45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
                   50                                  55                                  60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65                                  70                                  75                                  80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
                   85                                  90                                  95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
                   100                                  105                                  110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
                   115                                  120                                  125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
                   130                                  135                                  140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 48  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modified frag.; YFPF2A with Q69K mutation

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 48  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg aag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Lys Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110  
 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile

115	120	125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag			432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac			480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
145	150	155	160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc			528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc			576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu			
180	185	190	
ggc atg gac gag ctg tac aag			597
Gly Met Asp Glu Leu Tyr Lys			
195			
<210>	49		
<211>	199		
<212>	PRT		
<213>	Artificial		
<220>			
<223>	modified frag.; YFPF2A with Q69K mutation		
<400>	49		
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
1	5	10	15
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Lys Cys Phe			
20	25	30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala			
35	40	45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
50	55	60	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
65	70	75	80
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
85	90	95	
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
100	105	110	

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 50  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modified frag.; YFPF2A with Q69K mutation + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 50  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg aag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Lys Cys  
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly

85										90					95					
aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	336				
Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val					
		100						105					110							
tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	384				
Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys					
		115					120					125								
atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	432				
Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr					
	130					135					140									
cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	480				
Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn					
145					150				155					160						
cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	528				
His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys					
			165						170					175						
cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	576				
Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr					
			180					185					190							
ctc	ggc	atg	gac	gag	ctg	tac	aag									600				
Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys													
		195					200													

<210> 51

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modified frag.; YFPF2A with Q69K mutation + Met @ posit. 1

<400> 51

Met	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro
1				5					10					15	

Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	Gly	Tyr	Gly	Leu	Lys	Cys
			20					25					30		

Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser
		35					40					45			

Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp
	50					55					60				

Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr
65					70					75				80	

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 52  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modified frag.; citrine F2A , V68L/ Q69K mutations

<220>  
<221> CDS  
<222> (1)..(597)

<400> 52  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe  
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp

50	55	60	
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg			240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
65	70	75	80
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac			288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
	85	90	95
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat			336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
	100	105	110
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc			384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile			
	115	120	125
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag			432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
	130	135	140
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac			480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
	145	150	155
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc			528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
	165	170	175
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc			576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu			
	180	185	190
ggc atg gac gag ctg tac aag			597
Gly Met Asp Glu Leu Tyr Lys			
	195		
<210> 53			
<211> 199			
<212> PRT			
<213> Artificial			
<220>			
<223> modified frag.; citrine F2A , V68L/ Q69K mutations			
<400> 53			
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
1	5	10	15
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe			
	20	25	30
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala			
	35	40	45



Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 54  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; citrine F2A , V68L/ Q69K mutations + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 54  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc	96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys	
20 25 30	
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
100 105 110	
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 55

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; citrine F2A , V68L/ Q69K mutations + Met @ posit. 1

<400> 55

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys  
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 56

<211> 597

<212> DNA

<213> Artificial

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<220>
<223>  modif. frag.;citrine/VenusF2A, V68L/Q69K/N146I/M153T/V163A
        mutations

<220>
<221>  CDS
<222>  (1)..(597)

<400>  56
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg      48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1          5          10          15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc ttc      96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe
          20          25          30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
          35          40          45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
          50          55          60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65          70          75          80

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
          85          90          95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
          100          105          110

atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc      384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
          115          120          125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
          130          135          140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145          150          155          160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
          165          170          175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
          180          185          190

ggc atg gac gag ctg tac aag      597
Gly Met Asp Glu Leu Tyr Lys
          195

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<210> 57  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.;citrine/VenusF2A, V68L/Q69K/N146I/M153T/V163A  
 mutations

<400> 57

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe  
 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 58

<211> 600

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine/Venus F2A V68L/Q69K/N146I/M153T/V163A  
mutations + Met @ posit. 1

<220>

<221> CDS

<222> (1)..(600)

<400> 58

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
1 5 10 15	

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc	96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys	
20 25 30	

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
100 105 110	

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
115 120 125	

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
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His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
                   180                                  185                                  190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
                   195                                  200

<210> 59  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine/Venus F2A V68L/Q69K/N146I/M153T/V163A  
           mutations + Met @ posit. 1

<400> 59

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1                                  5                                  10                                  15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys  
                   20                                  25                                  30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
                   35                                  40                                  45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
                   50                                  55                                  60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65                                  70                                  75                                  80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
                   85                                  90                                  95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
                   100                                  105                                  110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
                   115                                  120                                  125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
                   130                                  135                                  140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145                                  150                                  155                                  160



His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 60  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2A, F64L mutation

<220>  
<221> CDS  
<222> (1)..(597)

<400> 60  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15  
ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe  
20 25 30  
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45  
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60  
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80  
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95  
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110  
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125  
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln

130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac			480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
145	150	155	160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc			528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
	165	170	175
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc			576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu			
	180	185	190
ggc atg gac gag ctg tac aag			597
Gly Met Asp Glu Leu Tyr Lys			
	195		
<210>	61		
<211>	199		
<212>	PRT		
<213>	Artificial		
<220>			
<223>	modif. frag.; CFP F2A, F64L mutation		
<400>	61		
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
1	5	10	15
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe			
	20	25	30
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala			
	35	40	45
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
	50	55	60
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
65	70	75	80
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
	85	90	95
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
	100	105	110
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile			
	115	120	125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 62  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, F64L mutation + Met @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 62  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys  
 20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

100

105

110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	384
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	432
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	480
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	528
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	576
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600

<210> 63  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, F64L mutation + Met @ posit. 1  
 <400> 63

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys 20 25 30
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 64  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2A , Y66W mutation

<220>  
<221> CDS  
<222> (1)..(597)

<400> 64  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15  
ccc tgg ccc acc ctg gtg acc acc ttc ggc tgg ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys Phe  
20 25 30  
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45  
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60  
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu

65	70	75	80	
gtg aac cgc atc	gag ctg aag ggc atc	gac ttc aag gag gac ggc aac		288
Val Asn Arg Ile	Glu Leu Lys Gly Ile	Asp Phe Lys Glu Asp Gly Asn		
	85	90	95	
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat				336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr				
	100	105	110	
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc				384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile				
	115	120	125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag				432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln				
	130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac				480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His				
	145	150	155	160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc				528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg				
	165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc				576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu				
	180	185	190	
ggc atg gac gag ctg tac aag				597
Gly Met Asp Glu Leu Tyr Lys				
	195			

<210> 65  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A , Y66W mutation

<400> 65

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys Phe
20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 66  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2A , Y66W mutation + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 66  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tgg ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser



35	40	45	
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60			192
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80			240
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95			288
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110			336
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125			384
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140			432
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160			480
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175			528
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190			576
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200			600

<210> 67  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A , Y66W mutation + Met @ posit. 1

<400> 67

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 68  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A , S65A mutation

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 68  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val

48

1	5	10	15	
ccc tgg ccc acc ctc gtg acc acc ttc gcc tac ggc ctg cag tgc ttc				96
Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys Phe	20	25	30	
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc				144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	35	40	45	
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac				192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	50	55	60	
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg				240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	65	70	75	80
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac				288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	85	90	95	
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat				336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	100	105	110	
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc				384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	115	120	125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag				432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac				480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	145	150	155	160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc				528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc				576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	180	185	190	
ggc atg gac gag ctg tac aag				597
Gly Met Asp Glu Leu Tyr Lys	195			

<210> 69  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A , S65A mutation

<400> 69

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys Phe  
20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 70

<211> 600

<212> DNA

<213> Artificial

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<220>
<223>  modif. frag.; CFP F2A , S65A  mutation + Met @ posit 1

<220>
<221>  CDS
<222>  (1)..(600)

<400>  70
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc      48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1                               5                               10                               15

gtg ccc tgg ccc acc ctc gtg acc acc ttc gcc tac ggc ctg cag tgc      96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys
                               20                               25                               30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
                               35                               40                               45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
                               50                               55                               60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                               70                               75                               80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                               85                               90                               95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
                               100                              105                              110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
                               115                              120                              125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                               130                              135                              140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                              150                              155                              160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                               165                              170                              175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
                               180                              185                              190

ctc ggc atg gac gag ctg tac aag                                     600
Leu Gly Met Asp Glu Leu Tyr Lys
                               195                               200

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<210> 71  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A , S65A mutation + Met @ posit 1  
 <400> 71

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys

<210> 72  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, S65A/Y66W/T203Y mutations

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 72  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ttc gcc tgg ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110  
 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125  
 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
 tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
                   180                  185                  190

ggc atg gac gag ctg tac aag 597  
 Gly Met Asp Glu Leu Tyr Lys  
                   195

<210> 73  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, S65A/Y66W/T203Y mutations

<400> 73

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1                  5                  10                  15

Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys Phe  
                   20                  25                  30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
                   35                  40                  45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
                   50                  55                  60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65                  70                  75                  80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
                   85                  90                  95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
                   100                  105                  110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
                   115                  120                  125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
                   130                  135                  140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145                  150                  155                  160



Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 74  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CGFP F2A, S65A/Y66W/T203Y mutations + Met @ pos. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 74  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ttc gcc tgg ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80  
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95  
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110  
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125  
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

130	135	140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac			480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn			
145	150	155	160
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag			528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys			
	165	170	175
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act			576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr			
	180	185	190
ctc ggc atg gac gag ctg tac aag			600
Leu Gly Met Asp Glu Leu Tyr Lys			
	195	200	
<210> 75			
<211> 200			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; CGFP F2A, S65A/Y66W/T203Y mutations + Met @ pos. 1			
<400> 75			
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro			
1	5	10	15
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys			
	20	25	30
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser			
	35	40	45
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp			
	50	55	60
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr			
65	70	75	80
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly			
	85	90	95
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val			
	100	105	110
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys			
	115	120	125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 76  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag. CGFP F2A , F64L/S65T/Y66W/M153T/V163A/T203Y  
 mutations

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 76  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
100 105 110	
atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
115 120 125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
130 135 140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
145 150 155 160	
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
165 170 175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
180 185 190	
ggc atg gac gag ctg tac aag	597
Gly Met Asp Glu Leu Tyr Lys	
195	

<210> 77  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag. CGFP F2A , F64L/S65T/Y66W/M153T/V163A/T203Y  
 mutations

<400> 77

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
1 5 10 15	
Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe	
20 25 30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
35 40 45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
50 55 60	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
65 70 75 80	

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 78  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag. CGFP F2A, F64L/S65T/Y66W/M153T/V163A/T203Y  
mutations + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 78  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys  
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
100 105 110	
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 79  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag. CGFP F2A, F64L/S65T/Y66W/M153T/V163A/T203Y  
 mutations + Met @ posit. 1

<400> 79

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 80

<211> 597

<212> DNA

<213> Artificial

<220>

<223> modif. frag., CFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A  
 mutations

<220>

<221> CDS

<222> (1)..(597)

<400> 80  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
 100 105 110  
 atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc 384  
 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
 115 120 125  
 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
 tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175  
 gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190  
 ggc atg gac gag ctg tac aag 597  
 Gly Met Asp Glu Leu Tyr Lys  
 195  
 <210> 81  
 <211> 199  
 <212> PRT  
 <213> Artificial



<220>

<223> modif. frag., CFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A  
mutations

<400> 81

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe  
20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 82

<211> 600

<212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag. CFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A  
 mutations + Met @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 82  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

gtg ccc tgg ccc acc ctg ctg acc acc ctg acc tgg ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys  
 20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 100 105 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctg gcc gac cac tac 432  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

ctc ggc atg gac gag ctg tac aag  
 Leu Gly Met Asp Glu Leu Tyr Lys  
           195                          200

600

<210> 83  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag. CFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A  
           mutations + Met @ posit. 1

<400> 83

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
   1                  5                  10                  15

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys  
                   20                  25                  30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
           35                          40                  45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
   50                          55                  60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
   65                  70                  75                  80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
                   85                  90                  95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
                   100                  105                  110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
           115                  120                  125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
   130                          135                  140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
   145                  150                  155                  160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
                   165                  170                  175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 84  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag. CFP F2A, N146I mutation

<220>  
<221> CDS  
<222> (1)..(597)

<400> 84  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15  
ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
20 25 30  
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45  
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60  
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80  
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95  
atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336  
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
100 105 110  
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125  
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140  
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

tac	ctg	agc	acc	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	528
Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	
				165					170					175		

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
                   180                  185                  190

ggc atg gac gag ctg tac aag 597  
 Gly Met Asp Glu Leu Tyr Lys  
                   195

<210> 85  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag. CFP F2A, N146I mutation

<400> 85

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1                  5                  10                  15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
                   20                  25                  30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
                   35                  40                  45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
                   50                  55                  60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65                  70                  75                  80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
                   85                  90                  95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
                   100                  105                  110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
                   115                  120                  125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
                   130                  135                  140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145                  150                  155                  160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 86  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag. CFP F2A, N146I mutation + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 86  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80  
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95  
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
100 105 110  
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125  
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

130	135	140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac			480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn			
145	150	155	160
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag			528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys			
	165	170	175
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act			576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr			
	180	185	190
ctc ggc atg gac gag ctg tac aag			600
Leu Gly Met Asp Glu Leu Tyr Lys			
	195	200	

<210> 87  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag. CFP F2A, N146I mutation + Met @ posit. 1

<400> 87

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125



Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 88  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag. CFP F2A, M153T mutation

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 88  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr

100

105

110

atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125	384
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140	432
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160	480
tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175	528
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190	576
ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys 195	597

<210> 89  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag. CFP F2A, M153T mutation

<400> 89

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1 5 10 15
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 90  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag. CFP F2A, M153T mutation + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 90  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80	240
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	288
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110	336
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	384
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	432
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	480
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	528
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	576
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600

<210> 91  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag. CFP F2A, M153T mutation + Met @ posit. 1

<400> 91

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 92  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag. CFP F2A, N146I/ M153T mutations

<220>  
<221> CDS  
<222> (1)..(597)

<400> 92  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

20										25					30					
gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	cac	gac	ttc	ttc	aag	tcc	gcc	144				
Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala					
		35					40					45								
atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	192				
Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp					
	50					55					60									
ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	240				
Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu					
65					70					75					80					
gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	288				
Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn					
				85					90					95						
atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	atc	agc	cac	aac	gtc	tat	336				
Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr					
			100					105					110							
atc	acc	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc	384				
Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile					
		115					120					125								
cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	432				
Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln					
	130					135					140									
cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	480				
Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His					
145					150					155					160					
tac	ctg	agc	acc	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	528				
Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg					
				165					170					175						
gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	576				
Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu					
			180					185					190							
ggc	atg	gac	gag	ctg	tac	aag										597				
Gly	Met	Asp	Glu	Leu	Tyr	Lys														
		195																		
<210> 93																				
<211> 199																				
<212> PRT																				
<213> Artificial																				
<220>																				
<223> modif. frag. CFP F2A, N146I/ M153T mutations																				
<400> 93																				
Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val					
1				5				10					15							

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 94  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag. CFP F2A, N146I/ M153T mutations + Met @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)



<400> 94

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
1 5 10 15	
gtg ccc tgg ccc acc ctg ctg acc acc ttc ggc tac ggc ctg cag tgc	96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
20 25 30	
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
100 105 110	
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctg gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 95  
 <211> 200  
 <212> PRT  
 <213> Artificial  
  
 <220>  
 <223> modif. frag. CFP F2A, N146I/ M153T mutations + Met @ posit. 1  
  
 <400> 95  
  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15  
  
 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30  
  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95  
  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 100 105 110  
  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125  
  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140  
  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160  
  
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175  
  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190  
  
 Leu Gly Met Asp Glu Leu Tyr Lys

<210> 96  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, F64L/S65T/Y66W/N146I/M153T  
 mutations

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 96  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ctc acc tgg ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
 100 105 110  
 atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125  
 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
 tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg

	165		170		175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc						576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu						
	180		185		190	
ggc atg gac gag ctg tac aag						597
Gly Met Asp Glu Leu Tyr Lys						
	195					
<210>	97					
<211>	199					
<212>	PRT					
<213>	Artificial					
<220>						
<223>	modif. frag.; CFP F2A, F64L/S65T/Y66W/N146I/M153T mutations					
<400>	97					
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val						
1	5		10		15	
Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe						
	20		25		30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala						
	35		40		45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp						
	50		55		60	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu						
65		70		75		80
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn						
	85		90		95	
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr						
	100		105		110	
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile						
	115		120		125	
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln						
	130		135		140	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His						
145		150		155		160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 98  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2A, F64L/S65T/Y66W/N146I/M153T  
mutations + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 98  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ctc acc tgg ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80  
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95  
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
100 105 110  
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384  
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 99  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, F64L/S65T/Y66W/N146I/M153T  
 mutations + Met @ posit. 1

<400> 99

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
1 5 10 15	
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys	
20 25 30	
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
100 105 110	

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 100  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, V163A mutation

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 100  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
85 90 95	
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat	336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	
100 105 110	
atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc	384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	
115 120 125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
130 135 140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
145 150 155 160	
tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
165 170 175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
180 185 190	
ggc atg gac gag ctg tac aag	597
Gly Met Asp Glu Leu Tyr Lys	
195	

<210> 101  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, V163A mutation

<400> 101

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
1 5 10 15	
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
20 25 30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
35 40 45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
50 55 60	



Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 102  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2A, V163A mutation + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 102  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser

35	40	45	
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac			192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp			
50	55	60	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc			240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr			
65	70	75	80
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc			288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly			
	85	90	95
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc			336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val			
	100	105	110
tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag			384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys			
	115	120	125
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac			432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr			
	130	135	140
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac			480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn			
145	150	155	160
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag			528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys			
	165	170	175
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act			576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr			
	180	185	190
ctc ggc atg gac gag ctg tac aag			600
Leu Gly Met Asp Glu Leu Tyr Lys			
	195	200	

<210> 103  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, V163A mutation + Met @ posit. 1

<400> 103

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 104  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, N146I/ V163A mutations

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 104  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val

48

1	5	10	15	
ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc				96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	20	25	30	
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc				144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	35	40	45	
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac				192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	50	55	60	
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg				240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	65	70	75	80
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac				288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	85	90	95	
atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat				336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	100	105	110	
atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc				384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	115	120	125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag				432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac				480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	145	150	155	160
tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc				528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc				576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	180	185	190	
ggc atg gac gag ctg tac aag				597
Gly Met Asp Glu Leu Tyr Lys	195			

<210> 105  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, N146I/ V163A mutations

<400> 105

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys

<210> 106  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, N146I/V163A mutations + Met @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 106  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15  
 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30  
 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95  
 aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 100 105 110  
 tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384  
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125  
 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160  
 cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
                   180                  185                  190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
                   195                  200

<210> 107  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, N146I/V163A mutations + Met @ posit. 1  
 <400> 107

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1                  5                  10                  15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
                   20                  25                  30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
                   35                  40                  45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
                   50                  55                  60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65                  70                  75                  80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
                   85                  90                  95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
                   100                  105                  110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
                   115                  120                  125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
                   130                  135                  140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145                  150                  155                  160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 108  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2A, M153T/V163A mutations

<220>  
<221> CDS  
<222> (1)..(597)

<400> 108  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15  
ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
20 25 30  
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45  
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60  
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80  
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95  
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110  
atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc 384  
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
115 120 125  
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln



130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac			480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
145	150	155	160
tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc			528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
	165	170	175
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc			576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu			
	180	185	190
ggc atg gac gag ctg tac aag			597
Gly Met Asp Glu Leu Tyr Lys			
	195		
<210> 109			
<211> 199			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; CFP F2A, M153T/V163A mutations			
<400> 109			
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
1	5	10	15
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe			
	20	25	30
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala			
	35	40	45
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
	50	55	60
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
65	70	75	80
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
	85	90	95
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
	100	105	110
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile			
	115	120	125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 110

<211> 600

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2A, M153T/V163A mutations + Met @ posit. 1

<220>

<221> CDS

<222> (1)..(600)

<400> 110

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc	48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
1 5 10 15	

gtg ccc tgg ccc acc ctg gtg acc acc ttc ggc tac ggc ctg cag tgc	96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
20 25 30	

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	

100	105	110	
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag			384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys			
115	120	125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac			432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr			
130	135	140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac			480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn			
145	150	155	160
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag			528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys			
165	170	175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act			576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr			
180	185	190	
ctc ggc atg gac gag ctg tac aag			600
Leu Gly Met Asp Glu Leu Tyr Lys			
195	200		

<210> 111  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, M153T/V163A mutations + Met @ posit. 1

<400> 111

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 112  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, N146I/M153T/V163A mutations

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 112  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctg gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu

65	70	75	80	
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac				288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	85	90	95	
atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat				336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	100	105	110	
atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc				384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	115	120	125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag				432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac				480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	145	150	155	160
tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc				528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc				576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	180	185	190	
ggc atg gac gag ctg tac aag				597
Gly Met Asp Glu Leu Tyr Lys	195			

<210> 113  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2A, N146I/M153T/V163A mutations

<400> 113

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
1	5	10	15
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe			
20	25	30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala			
35	40	45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
50	55	60	

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 114  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2A, N146I/M153T/V163A mutations  
and Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 114  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
100 105 110	
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 115

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2A, N146I/M153T/V163A mutations  
and Met added @ posit. 1

<400> 115

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200



<210> 116  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A/T203Y mutations

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 116  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctg gtg acc acc ctg acc tgg ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
 100 105 110  
 atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc 384  
 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
 115 120 125  
 cgc cac aac atc gag gac ggc agc gtg cag ctg gcc gac cac tac cag 432  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
 tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
                   180                                  185                                  190

ggc atg gac gag ctg tac aag 597  
 Gly Met Asp Glu Leu Tyr Lys  
                   195

<210> 117  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A/T203Y  
           mutations

<400> 117

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1                                  5                                  10                                  15

Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe  
                   20                                  25                                  30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
                   35                                  40                                  45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
                   50                                  55                                  60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65                                  70                                  75                                  80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
                   85                                  90                                  95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
                   100                                  105                                  110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
                   115                                  120                                  125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
                   130                                  135                                  140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145                                  150                                  155                                  160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 118  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag., CGFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A/T203Y  
mutations and Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 118  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80  
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95  
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
100 105 110  
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384  
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 119  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag., CGFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A/T203Y  
 mutations and Met added @ posit. 1

<400> 119

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
1 5 10 15	
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys	
20 25 30	
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
100 105 110	

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 120  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, N146I/T203Y mutations

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 120  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctg gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn

				85					90					95					
atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	atc	agc	cac	aac	gtc	tat		336		
Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr				
				100					105					110					
atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc		384		
Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile				
				115					120					125					
cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag		432		
Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln				
				130					135					140					
cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac		480		
Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His				
				145					150					155					
tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc		528		
Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg				
				165					170					175					
gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc		576		
Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu				
				180					185					190					
ggc	atg	gac	gag	ctg	tac	aag											597		
Gly	Met	Asp	Glu	Leu	Tyr	Lys													
				195															

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 122  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CGFP F2A, N146I/T203Y mutations + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 122  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp

50

55

60



gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80	240
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	288
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110	336
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	384
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	432
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	480
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	528
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	576
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600

<210> 123

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CGFP F2A, N146I/T203Y mutations + Met @ posit. 1

<400> 123

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15
--

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30
---

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45
---

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 124  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CGFP F2A, M153T/T203Y mutations

<220>  
<221> CDS  
<222> (1)..(597)

<400> 124  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

20	25	30	
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45			144
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60			192
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80			240
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95			288
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110			336
atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125			384
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140			432
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160			480
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175			528
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190			576
ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys 195			597

<210> 125

<211> 199

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CGFP F2A, M153T/T203Y mutations

<400> 125

Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val
1				5					10					15	

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
                     20                    25                    30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
                     35                    40                    45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
                     50                    55                    60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
                     65                    70                    75                    80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
                     85                    90                    95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
                     100                    105                    110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
                     115                    120                    125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
                     130                    135                    140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
                     145                    150                    155                    160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
                     165                    170                    175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
                     180                    185                    190

Gly Met Asp Glu Leu Tyr Lys  
                     195

<210> 126  
 <211> 600  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> modif. frag.; CGFP F2A, M153T/T203Y mutations + Met @ posit. 1  
  
 <220>  
 <221> CDS  
 <222> (1)..(600)  
  
 <400> 126  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15  
  
 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30  
  
 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
  
 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95  
  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110  
  
 tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125  
  
 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140  
  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160  
  
 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175  
  
 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr



Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 128  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CGFP F2A,N146I/ M153T/T203Y mutations

<220>  
<221> CDS  
<222> (1)..(597)

<400> 128  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336  
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
100 105 110

atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

ggc atg gac gag ctg tac aag 597  
 Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 129  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A,N146I/ M153T/T203Y mutations

<400> 129

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125



Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 130  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A,N146I/ M153T/T203Y mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 130  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15  
 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30  
 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
100 105 110	
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 131  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A,N146I/ M153T/T203Y mutations  
 and Met added @ posit. 1

<400> 131

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
1 5 10 15	
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
20 25 30	
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 132  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CGFP F2A,F64L/S65T/Y66W/N146I/M153T/T203Y  
mutations

<220>  
<221> CDS  
<222> (1)..(597)

<400> 132  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe  
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
50 55 60	
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
65 70 75 80	
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
85 90 95	
atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat	336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr	
100 105 110	
atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
115 120 125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
130 135 140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
145 150 155 160	
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
165 170 175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
180 185 190	
ggc atg gac gag ctg tac aag	597
Gly Met Asp Glu Leu Tyr Lys	
195	

<210> 133

<211> 199

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CGFP F2A, F64L/S65T/Y66W/N146I/M153T/T203Y mutations

<400> 133

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe
20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 134  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, F64L/S65T/Y66W/N146I/M153T/T203Y  
 mutations and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 134  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc

48

Met	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro		
1				5					10					15			
gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg	acc	tgg	ggc	ctg	cag	tgc		96
Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Trp	Gly	Leu	Gln	Cys		
			20					25					30				
ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	cac	gac	ttc	ttc	aag	tcc		144
Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser		
		35					40					45					
gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac		192
Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp		
	50					55					60						
gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc		240
Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr		
65					70					75					80		
ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc		288
Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly		
				85					90					95			
aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	atc	agc	cac	aac	gtc		336
Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser	His	Asn	Val		
			100					105					110				
tat	atc	acc	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag		384
Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys		
		115					120					125					
atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac		432
Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr		
	130					135					140						
cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac		480
Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn		
145					150					155					160		
cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag		528
His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys		
				165					170					175			
cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act		576
Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr		
			180					185					190				
ctc	ggc	atg	gac	gag	ctg	tac	aag										600
Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys										
		195					200										

<210> 135  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, F64L/S65T/Y66W/N146I/M153T/T203Y  
 mutations and Met added @ posit. 1

<400> 135

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 136  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, V163A/T203Y mutations

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 136  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctg gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110  
 atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc 384  
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
 115 120 125  
 cgc cac aac atc gag gac ggc agc gtg cag ctg gcc gac cac tac cag 432  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
 tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg



	165		170		175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc						576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu						
	180		185		190	
ggc atg gac gag ctg tac aag						597
Gly Met Asp Glu Leu Tyr Lys						
	195					
<210>	137					
<211>	199					
<212>	PRT					
<213>	Artificial					
<220>						
<223>	modif. frag.; CGFP F2A, V163A/T203Y mutations					
<400>	137					
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val						
1	5		10		15	
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe						
	20		25		30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala						
	35		40		45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp						
	50		55		60	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu						
65		70		75		80
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn						
	85		90		95	
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr						
	100		105		110	
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile						
	115		120		125	
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln						
	130		135		140	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His						
145		150		155		160

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Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 138  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
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<220>  
<221> CDS  
<222> (1)..(600)

<400> 138  
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Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80  
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95  
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110  
tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
115 120 125  
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

130	135	140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac			480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn			
145	150	155	160
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag			528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys			
	165	170	175
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act			576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr			
	180	185	190
ctc ggc atg gac gag ctg tac aag			600
Leu Gly Met Asp Glu Leu Tyr Lys			
	195	200	

<210> 139

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CGFP F2A, V163A/T203Y mutations + Met @ posit. 1

<400> 139

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 140  
 <211> 597  
 <212> DNA  
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<220>  
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<220>  
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 <222> (1)..(597)

<400> 140  
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 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctg gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr

100	105	110	
atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc			384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile			
115	120	125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag			432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac			480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
145	150	155	160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc			528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc			576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu			
180	185	190	
ggc atg gac gag ctg tac aag			597
Gly Met Asp Glu Leu Tyr Lys			
195			

<210> 141  
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 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, N146I/V163A/T203Y mutations

<400> 141

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 142  
<211> 600  
<212> DNA  
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<220>  
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and Met added @ posit. 1

<220>  
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<222> (1)..(600)

<400> 142  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384  
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 143  
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 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, N146I/V163A/T203Y mutations  
 and Met added @ posit. 1

<400> 143

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45



Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 144  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CGFP F2A, M153T/V163A/T203Y mutations

<220>  
<221> CDS  
<222> (1)..(597)

<400> 144  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

20										25										30										
gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	cac	gac	ttc	ttc	aag	tcc	gcc	144														
Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala															
		35					40					45																		
atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	192														
Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp															
	50					55					60																			
ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	240														
Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu															
65					70					75					80															
gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	288														
Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn															
			85					90						95																
atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	tat	336														
Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr															
			100					105						110																
atc	acc	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gcc	aac	ttc	aag	atc	384														
Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile															
		115					120					125																		
cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	432														
Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln															
	130					135					140																			
cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	480														
Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His															
145					150					155					160															
tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	528														
Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg															
				165					170					175																
gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	576														
Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu															
			180					185					190																	
ggc	atg	gac	gag	ctg	tac	aag										597														
Gly	Met	Asp	Glu	Leu	Tyr	Lys																								
		195																												
<210> 145																														
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<213> Artificial																														
<220>																														
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<400> 145																														
Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val															
1				5					10					15																

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 146  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
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 and Met added @ posit. 1

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 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30  
 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110  
 tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125  
 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160  
 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 147  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, N146I/V163A/T203Y mutations  
 and Met added @ posit. 1

<400> 147

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 148  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CGFP F2A, N146I/M153T/V163A/T203Y mutations

<220>  
<221> CDS  
<222> (1)..(597)

<400> 148  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15  
ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
20 25 30  
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45  
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60  
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80  
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95  
atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336  
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
100 105 110  
atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc 384  
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
115 120 125  
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

ggc atg gac gag ctg tac aag 597  
 Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 149  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, N146I/M153T/V163A/T203Y mutations

<400> 149

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr  
 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
 115 120 125





Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 150  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, N146I/M153T/V163A/T203Y  
 mutations and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 150  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15  
 gtg ccc tgg ccc acc ctg gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30  
 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val	
100 105 110	
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 151  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2A, N146I/M153T/V163A/T203Y  
 mutations and Met added @ posit. 1

<400> 151

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
1 5 10 15	
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys	
20 25 30	
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 152  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; BFP (blue) F2A, Y66H mutation

<220>  
<221> CDS  
<222> (1)..(597)

<400> 152  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys Phe  
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp

50	55	60	
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg			240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
65	70	75	80
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac			288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
	85	90	95
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat			336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
	100	105	110
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc			384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile			
	115	120	125
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag			432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
	130	135	140
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac			480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
	145	150	155
tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc			528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
	165	170	175
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc			576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu			
	180	185	190
ggc atg gac gag ctg tac aag			597
Gly Met Asp Glu Leu Tyr Lys			
	195		
<210> 153			
<211> 199			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; BFP (blue) F2A, Y66H mutation			
<400> 153			
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
1	5	10	15
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys Phe			
	20	25	30
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala			
	35	40	45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 154  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; BFP (blue) F2A, Y66H mutation and Met added  
@ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 154  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc 96

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys  
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc	144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac	192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
65 70 75 80	
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
100 105 110	
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 155

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP (blue) F2A, Y66H mutation and Met added  
@ posit. 1

<400> 155

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys  
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200



<210> 156  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP (blue) F2A, Y145F mutation

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 156

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
1 5 10 15	
ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc	96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe	
20 25 30	
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc	144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	
35 40 45	
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
50 55 60	
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
65 70 75 80	
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac	288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	
85 90 95	
atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc tat	336
Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr	
100 105 110	
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc	384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile	
115 120 125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag	432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln	
130 135 140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac	480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	
145 150 155 160	
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
165 170 175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	

180 185 190  
 ggc atg gac gag ctg tac aag  
 Gly Met Asp Glu Leu Tyr Lys  
 195  
 597  
 <210> 157  
 <211> 199  
 <212> PRT  
 <213> Artificial  
 <220>  
 <223> modif. frag.; BFP (blue) F2A, Y145F mutation  
 <400> 157  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr  
 100 105 110  
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 158

<211> 600

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP (blue) F2A, Y145F mutation and Met added  
@ posit. 1

<220>

<221> CDS

<222> (1)..(600)

<400> 158

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

gtg ccc tgg ccc acc ctg ctg acc acc ttc ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc 336  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val  
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 159

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP (blue) F2A, Y145F mutation and Met added  
 @ posit. 1

<400> 159

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 160  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP (blue) F2A, Y66H/Y145F mutations

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 160  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctg gtg acc acc ttc ggc cac ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr

100	105	110	
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc			384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile			
115	120	125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag			432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac			480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
145	150	155	160
tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc			528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc			576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu			
180	185	190	
ggc atg gac gag ctg tac aag			597
Gly Met Asp Glu Leu Tyr Lys			
195			

<210> 161

<211> 199

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP (blue) F2A, Y66H/Y145F mutations

<400> 161

Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val
1				5					10					15	

Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	Gly	His	Gly	Leu	Gln	Cys	Phe
			20					25					30		

Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala
		35					40					45			

Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp
	50					55					60				

Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu
65					70					75					80

Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn
				85					90					95	

Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 162  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; BFP (blue) F2A, Y66H/Y145F mutations  
and Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 162  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctg gtg acc acc ttc ggc cac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys  
20 25 30  
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80



ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
85 90 95	
aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc	336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val	
100 105 110	
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 163  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP (blue) F2A, Y66H/Y145F mutations  
 and Met added @ posit. 1

<400> 163

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro	
1 5 10 15	
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys	
20 25 30	
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	
35 40 45	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	
50 55 60	

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val  
100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 164  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; BFP (blue) F2A,F64L/Y66H/Y145F mutations

<220>  
<221> CDS  
<222> (1)..(597)

<400> 164  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15  
ccc tgg ccc acc ctc gtg acc acc ctg ggc cac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly His Gly Leu Gln Cys Phe  
20 25 30  
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144

Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala		
		35					40					45					
atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac		192
Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp		
		50				55					60						
ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg		240
Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu		
		65			70					75					80		
gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac		288
Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn		
				85					90					95			
atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	ttc	aac	agc	cac	aac	gtc	tat		336
Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Phe	Asn	Ser	His	Asn	Val	Tyr		
			100					105					110				
atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc		384
Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile		
		115					120					125					
cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag		432
Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln		
		130				135					140						
cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac		480
Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His		
		145			150					155					160		
tac	ctg	agc	acc	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc		528
Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg		
				165					170					175			
gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc		576
Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu		
			180					185					190				
ggc	atg	gac	gag	ctg	tac	aag											597
Gly	Met	Asp	Glu	Leu	Tyr	Lys											
		195															

<210> 165  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP (blue) F2A,F64L/Y66H/Y145F mutations

<400> 165

Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val
1				5					10					15	

Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Gly	His	Gly	Leu	Gln	Cys	Phe
			20					25					30		



Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr  
 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

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<210> 166
<211> 600
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; BFP F2A, F64L/Y66H/Y145F mutations and Met added
      @ posit. 1

<220>
<221> CDS
<222> (1)..(600)

<400> 166
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc      48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1                               5                               10                               15

gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc cac ggc ctg cag tgc      96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly His Gly Leu Gln Cys
                20                               25                               30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
                35                               40                               45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
                50                               55                               60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                               70                               75                               80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                               90                               95

aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
                100                               105                               110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
                115                               120                               125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                130                               135                               140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                               150                               155                               160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                               170                               175

```

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 167  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F2A, F64L/Y66H/Y145F mutations and Met added  
 @ posit. 1

<400> 167

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly His Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 168  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; EGFP F2A, with Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 168  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15  
gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys  
20 25 30  
ttc tcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45  
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80  
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95  
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110  
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125  
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr



130	135	140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac			480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn			
145	150	155	160
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag			528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys			
	165	170	175
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act			576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr			
	180	185	190
ctc ggc atg gac gag ctg tac aag			600
Leu Gly Met Asp Glu Leu Tyr Lys			
	195	200	

<210> 169  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; EGFP F2A, with Met added @ posit. 1

<400> 169

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro			
1	5	10	15
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys			
	20	25	30
Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser			
	35	40	45
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp			
	50	55	60
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr			
	65	70	75
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly			
	85	90	95
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val			
	100	105	110
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys			
	115	120	125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 170  
 <211> 597  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; EGFP emerald F2A, S65T/S72A/N149K/M153T/I167T  
 mutations

<220>  
 <221> CDS  
 <222> (1)..(597)

<400> 170  
 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 ccc tgg ccc acc ctc gtg acc acc ttc acc tac ggc ctg cag tgc ttc 96  
 Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag gtc tat 336  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val Tyr  
 100 105 110  
  
 atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag acc 384  
 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr  
 115 120 125  
  
 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
  
 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
  
 tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175  
  
 gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190  
  
 ggc atg gac gag ctg tac aag 597  
 Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 171

<211> 199

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; EGFP emerald F2A, S65T/S72A/N149K/M153T/I167T mutations

<400> 171

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Leu Gln Cys Phe  
 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val Tyr  
100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr  
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 172

<211> 600

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; EGFP emerald F2A,S65T/S72A/N149K/M153T/I167T  
mutations and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(600)

<400> 172

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc acc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Leu Gln Cys  
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80	240
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	288
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val 100 105 110	336
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	384
acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	432
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	480
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	528
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	576
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600

<210> 173

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; EGFP emerald F2A,S65T/S72A/N149K/M153T/I167T  
mutations and Met added @ posit. 1

<400> 173

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15
--

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Leu Gln Cys 20 25 30
---

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45
---

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val  
100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 174  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F2A, Y203F mutation

<220>  
<221> CDS  
<222> (1)..(597)

<400> 174  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

	20	25	30	
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc				144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala				
	35	40	45	
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac				192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp				
	50	55	60	
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg				240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu				
	65	70	75	80
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac				288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn				
	85	90	95	
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat				336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr				
	100	105	110	
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc				384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile				
	115	120	125	
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag				432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln				
	130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac				480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His				
	145	150	155	160
tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc				528
Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg				
	165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc				576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu				
	180	185	190	
ggc atg gac gag ctg tac aag				597
Gly Met Asp Glu Leu Tyr Lys				
	195			
<210> 175				
<211> 199				
<212> PRT				
<213> Artificial				
<220>				
<223> modif. frag.; YFP F2A, Y203F mutation				
<400> 175				
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val				
1 5 10 15				



Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 176  
 <211> 600  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> modif. frag.; YFP F2A, Y203F mutation and Met added @ posit. 1  
  
 <220>  
 <221> CDS  
 <222> (1)..(600)  
  
 <400> 176  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15  
  
 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30  
  
 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
  
 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95  
  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110  
  
 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384  
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125  
  
 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140  
  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160  
  
 cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
                   180                  185                  190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
                   195                  200

<210> 177  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F2A, Y203F mutation and Met added @ posit. 1

<400> 177

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1                  5                  10                  15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
                   20                  25                  30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
                   35                  40                  45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
                   50                  55                  60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65                  70                  75                  80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
                   85                  90                  95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
                   100                  105                  110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
                   115                  120                  125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
                   130                  135                  140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145                  150                  155                  160

His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 178  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F2A, Y203H mutation

<220>  
<221> CDS  
<222> (1)..(597)

<400> 178  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15  
ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
20 25 30  
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Lys Ser Ala  
35 40 45  
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60  
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80  
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95  
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110  
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125  
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432  
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln

130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac			480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
145	150	155	160
tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc			528
Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
	165	170	175
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc			576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu			
	180	185	190
ggc atg gac gag ctg tac aag			597
Gly Met Asp Glu Leu Tyr Lys			
	195		
<210>	179		
<211>	199		
<212>	PRT		
<213>	Artificial		
<220>			
<223>	modif. frag.; YFP F2A, Y203H mutation		
<400>	179		
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
1	5	10	15
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe			
	20	25	30
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala			
	35	40	45
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
	50	55	60
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
65	70	75	80
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
	85	90	95
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
	100	105	110
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile			
	115	120	125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 180

<211> 600

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2A, Y203H mutation and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(600)

<400> 180

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

100	105	110	
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag			384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys			
115	120	125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac			432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr			
130	135	140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac			480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn			
145	150	155	160
cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag aag			528
His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys			
165	170	175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act			576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr			
180	185	190	
ctc ggc atg gac gag ctg tac aag			600
Leu Gly Met Asp Glu Leu Tyr Lys			
195	200		

<210> 181  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F2A, Y203H mutation and Met added @ posit. 1  
 <400> 181

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 182  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; SEYFP F2A frag(aa 40-239 of SEYFP), with  
 Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 182  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15  
 gtg ccc tgg ccc acc ctg gtg acc acc ctg ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys  
 20 25 30  
 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60



gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 432  
 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
 130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 183  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; SEYFP F2A frag(aa 40-239 of SEYFP, with  
 Met added @ posit. 1

<400> 183

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 184  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; Venus F2A, with S175G mutation

<220>  
<221> CDS  
<222> (1)..(597)

<400> 184  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

20										25										30										
gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	cac	gac	ttc	ttc	aag	tcc	gcc	144														
Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala															
		35					40						45																	
atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	192														
Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp															
	50					55					60																			
ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	240														
Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu															
65					70					75					80															
gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	288														
Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn															
			85					90						95																
atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	tat	336														
Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr															
			100					105						110																
atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc	384														
Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile															
		115					120					125																		
cgc	cac	aac	atc	gag	gac	ggc	ggc	gtg	cag	ctc	gcc	gac	cac	tac	cag	432														
Arg	His	Asn	Ile	Glu	Asp	Gly	Gly	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln															
	130					135					140																			
cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	480														
Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His															
145					150					155					160															
tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	528														
Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg															
				165					170					175																
gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	576														
Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu															
			180					185					190																	
ggc	atg	gac	gag	ctg	tac	aag										597														
Gly	Met	Asp	Glu	Leu	Tyr	Lys																								
		195																												
<210>	185																													
<211>	199																													
<212>	PRT																													
<213>	Artificial																													
<220>																														
<223>	modif. frag.;	Venus F2A,	with S175G	mutation																										
<400>	185																													
Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val															
1				5				10					15																	

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 115 120 125

Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 186  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2A, with S175G mutation and Met  
 added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 186  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15  
 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30  
 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110  
 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384  
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125  
 atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 432  
 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
 130 135 140  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160  
 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 187  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2A, with S175G mutation and Met  
 added @ posit. 1

<400> 187

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 188  
<211> 597  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; Venus F2A, with M153T, S175G mutations

<220>  
<221> CDS  
<222> (1)..(597)

<400> 188  
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15  
ccc tgg ccc acc ctg gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
20 25 30  
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45  
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60  
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80  
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288  
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95  
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336  
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110  
atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384  
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
115 120 125  
cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag 432  
Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln

130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac			480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
145	150	155	160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc			528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
	165	170	175
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc			576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu			
	180	185	190
ggc atg gac gag ctg tac aag			597
Gly Met Asp Glu Leu Tyr Lys			
	195		
<210>	189		
<211>	199		
<212>	PRT		
<213>	Artificial		
<220>			
<223>	modif. frag.; Venus F2A, with M153T, S175G mutations		
<400>	189		
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
1	5	10	15
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe			
	20	25	30
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala			
	35	40	45
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
	50	55	60
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
65	70	75	80
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
	85	90	95
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
	100	105	110
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile			
	115	120	125



Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190

Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 190  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2A, M153T, S175G mutations and Met  
 added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 190  
 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15  
 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30  
 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
115 120 125	
atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac	432
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
145 150 155 160	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
180 185 190	
ctc ggc atg gac gag ctg tac aag	600
Leu Gly Met Asp Glu Leu Tyr Lys	
195 200	

<210> 191  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif.frag.; Venus F2A, M153T, S175G mutations and Met  
 added @ posit. 1

<400> 191

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 192

<211> 597

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2A, with V163A, S175G mutations

<220>

<221> CDS

<222> (1)..(597)

<400> 192

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48  
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
1 5 10 15

ccc tgg ccc acc ctg gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96  
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144  
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192  
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240  
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu

65	70	75	80	
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac				288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	85	90	95	
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat				336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	100	105	110	
atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc				384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	115	120	125	
cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag				432
Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln	130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac				480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	145	150	155	160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc				528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc				576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	180	185	190	
ggc atg gac gag ctg tac aag				597
Gly Met Asp Glu Leu Tyr Lys	195			

<210> 193  
 <211> 199  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2A, with V163A, S175G mutations

<400> 193

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
115 120 125

Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln  
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
180 185 190

Gly Met Asp Glu Leu Tyr Lys  
195

<210> 194  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; Venus F2A, w. V163A, S175G mutations  
and Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(600)

<400> 194  
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48  
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96  
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110  
 tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384  
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125  
 atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 432  
 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
 130 135 140  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160  
 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175  
 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190  
 ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 195  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2A, w. V163A, S175G mutations  
 and Met added @ posit. 1

<400> 195

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys  
 20 25 30



Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
 195 200

<210> 196

<211> 597

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2A,F46L/F64L/M153T/V163A/S175G mutations

<220>

<221> CDS

<222> (1)..(597)

<400> 196

ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg  
 Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val

48

1	5	10	15	
ccc tgg ccc acc ctc gtg acc acc ctc ggc tac ggc ctg cag tgc ttc				96
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe	20	25	30	
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc				144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala	35	40	45	
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac				192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	50	55	60	
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg				240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	65	70	75	80
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac				288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	85	90	95	
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat				336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr	100	105	110	
atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc				384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile	115	120	125	
cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag				432
Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln	130	135	140	
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac				480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His	145	150	155	160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc				528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	165	170	175	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc				576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	180	185	190	
ggc atg gac gag ctg tac aag				597
Gly Met Asp Glu Leu Tyr Lys	195			

<210> 197

<211> 199

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2A,F46L/F64L/M153T/V163A/S175G mutations

<400> 197

Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val  
 1 5 10 15  
 Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe  
 20 25 30  
 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala  
 35 40 45  
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 50 55 60  
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 65 70 75 80  
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 85 90 95  
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 100 105 110  
 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile  
 115 120 125  
 Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln  
 130 135 140  
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 145 150 155 160  
 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 165 170 175  
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
 180 185 190  
 Gly Met Asp Glu Leu Tyr Lys  
 195

<210> 198  
 <211> 600  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2A, F46L/F64L/M153T/V163A/S175G  
 mutations and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 198  
 atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc 48  
 Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro  
 1 5 10 15  
 gtg ccc tgg ccc acc ctc gtg acc acc ctc ggc tac ggc ctg cag tgc 96  
 Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys  
 20 25 30  
 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144  
 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
 35 40 45  
 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192  
 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
 50 55 60  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65 70 75 80  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 85 90 95  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 100 105 110  
 tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 115 120 125  
 atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 432  
 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
 130 135 140  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145 150 155 160  
 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
                   180                                  185                                  190

ctc ggc atg gac gag ctg tac aag 600  
 Leu Gly Met Asp Glu Leu Tyr Lys  
                   195                                  200

<210> 199  
 <211> 200  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2A, F46L/F64L/M153T/V163A/S175G  
           mutations and Met added @ posit. 1

<400> 199

Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro  
 1                                  5                                  10                                  15

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys  
                   20                                  25                                  30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser  
                   35                                  40                                  45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
                   50                                  55                                  60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 65                                  70                                  75                                  80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
                   85                                  90                                  95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
                   100                                  105                                  110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
                   115                                  120                                  125

Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
                   130                                  135                                  140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 145                                  150                                  155                                  160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys  
195 200

<210> 200  
<211> 306  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1B (aa residues 1-103 of YFP) with  
posit. 1 Met removed

<220>  
<221> CDS  
<222> (1)..(306)

<400> 200  
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15  
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30  
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45  
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60  
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80  
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95  
acc atc ttc ttc aag gac 306  
Thr Ile Phe Phe Lys Asp  
100

<210> 201  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B (aa residues 1-103 of YFP) with  
 posit. 1 Met removed

<400> 201

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp  
 100

<210> 202  
 <211> 309  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is  
 T,  
 residue 69 is V, and residue 73 is S

<220>  
 <221> CDS  
 <222> (1)..(309)

<400> 202  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ctc acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac 309  
 Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 203  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is  
 T,  
 residue 69 is V, and residue 73 is S

<400> 203

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95



Arg Thr Ile Phe Phe Lys Asp  
100

<210> 204  
<211> 306  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is T,  
residue 69 is V, residue 73 is S, and posit. 1 Met has been removed

<220>  
<221> CDS  
<222> (1)..(306)

<400> 204  
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15  
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30  
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45  
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
50 55 60  
acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cgg 240  
Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80  
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95  
acc atc ttc ttc aag gac 306  
Thr Ile Phe Phe Lys Asp  
100

<210> 205  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is T,  
 residue 69 is V, residue 73 is S, and posit. 1 Met has been removed

<400> 205

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp  
 100

<210> 206  
 <211> 309  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with K79R mutation

<220>  
 <221> CDS  
 <222> (1)..(309)

<400> 206

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20										25					30					
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile					
35						40					45									
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr					
50			55						60											
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	cgc	240				
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Arg					
65					70					75					80					
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288				
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu					
				85					90					95						
cgc	acc	atc	ttc	ttc	aag	gac										309				
Arg	Thr	Ile	Phe	Phe	Lys	Asp														
100																				

<210> 207  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with K79R mutation

<400> 207

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
			35				40					45			
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Arg
65					70					75				80	
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
				85					90					95	
Arg	Thr	Ile	Phe	Phe	Lys	Asp									
100															

<210> 208  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with K79R mutation and  
 posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 208  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg 240  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac 306  
 Thr Ile Phe Phe Lys Asp  
 100

<210> 209  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with K79R mutation and  
 posit. 1 Met removed

<400> 209

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

20

25

30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp  
100

```
<210> 210
<211> 309
<212> DNA
<213> Artificial
```

<220>  
<223> modif. frag.; YFP F1B with Y66F mutation

```
<220>
<221> CDS
<222> (1) .. (309)
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<400>																210	
atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48	
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1				5					10					15			
<hr/>																	
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96	
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				
<hr/>																	
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144	
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
		35					40					45					
<hr/>																	
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192	
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
	50					55					60						
<hr/>																	
ttc	ggc	ttc	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240	
Phe	Gly	Phe	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65					70				75						80		
<hr/>																	
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288	
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
				85					90					95			

cgc acc atc ttc ttc aag gac  
 Arg Thr Ile Phe Phe Lys Asp  
 100

309

<210> 211  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with Y66F mutation

<400> 211

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 212  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with Y66F mutation and  
 posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 212

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val

48

1	5	10	15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag				96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	20	25	30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc				144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	35	40	45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc				192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	50	55	60	
ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg				240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	65	70	75	80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc				288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	85	90	95	
acc atc ttc ttc aag gac				306
Thr Ile Phe Phe Lys Asp	100			

<210> 213  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with Y66F mutation and  
 posit. 1 Met removed

<400> 213

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	1	5	10	15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	20	25	30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	50	55	60	
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	85	90	95	

Thr Ile Phe Phe Lys Asp  
100

<210> 214  
<211> 309  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1B with Q69K mutation

<220>  
<221> CDS  
<222> (1)..(309)

<400> 214  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
  
ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
  
cgc acc atc ttc ttc aag gac 309  
Arg Thr Ile Phe Phe Lys Asp  
100

<210> 215  
<211> 103  
<212> PRT  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1B with Q69K mutation

<400> 215

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15





Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp  
100

<210> 216  
<211> 306  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1B with Q69K mutation and  
posit. 1 Met removed

<220>  
<221> CDS  
<222> (1)...(306)

<400> 216  
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
                   85                                  90                                  95

acc atc ttc ttc aag gac 306  
 Thr Ile Phe Phe Lys Asp  
                   100

<210> 217  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with Q69K mutation and  
           posit. 1 Met removed

<400> 217

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1                  5                                  10                                  15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
                   20                                  25                                  30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
                   35                                  40                                  45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
           50                                  55                                  60

Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65                                  70                                  75                                  80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
                   85                                  90                                  95

Thr Ile Phe Phe Lys Asp  
                   100

<210> 218  
 <211> 309  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with K79R mutation

<220>  
 <221> CDS  
 <222> (1)..(309)

<400> 218  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc 240  
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg  
 65 70 75 80  
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac 309  
 Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 219  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with K79R mutation

<400> 219

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 220  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with K79R mutation and  
 posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 220  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg 240  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac 306

Thr Ile Phe Phe Lys Asp  
100

<210> 221  
<211> 102  
<212> PRT  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1B with K79R mutation and  
posit. 1 Met removed

<400> 221

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp  
100

<210> 222  
<211> 309  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; citrine F1B, with V68L, Q69M mutations

<220>  
<221> CDS  
<222> (1)..(309)

<400> 222

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac	309
Arg Thr Ile Phe Phe Lys Asp	
100	

<210> 223  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine F1B, with V68L, Q69M mutations

<400> 223

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
Arg Thr Ile Phe Phe Lys Asp	

100



<210> 224  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine F1B, with V68L, Q69M mutations  
 and posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 224  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac 306  
 Thr Ile Phe Phe Lys Asp  
 100

<210> 225  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine F1B, with V68L, Q69M mutations  
 and posit. 1 Met removed

<400> 225

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

	20		25		30											
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
	35						40					45				
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					
Gly	Tyr	Gly	Leu	Met	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65					70					75					80	
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95		
Thr	Ile	Phe	Phe	Lys	Asp											
				100												
<210>	226															
<211>	309															
<212>	DNA															
<213>	Artificial															
<220>																
<223>	modif. frag.; Venus F1B with F46L, F64L mutations															
<220>																
<221>	CDS															
<222>	(1)..(309)															
<400>	226															
atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ctg	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55			60							
ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75					80		
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95		

cgc acc atc ttc ttc aag gac  
 Arg Thr Ile Phe Phe Lys Asp  
 100

309

<210> 227  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F1B with F46L, F64L mutations

<400> 227

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 228  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F1B with F46L, F64L mutations  
 and posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 228

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val

48

1	5	10	15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag				96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu				
	20	25	30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc				144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys				
	35	40	45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg				192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu				
	50	55	60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg				240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg				
	65	70	75	80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc				288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg				
	85	90	95	
acc atc ttc ttc aag gac				306
Thr Ile Phe Phe Lys Asp				
	100			

<210> 229  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F1B with F46L, F64L mutations  
 and posit. 1 Met removed

<400> 229

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val				
1	5	10	15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu				
	20	25	30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys				
	35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu				
	50	55	60	
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg				
	65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg				
	85	90	95	

Thr Ile Phe Phe Lys Asp  
100

<210> 230  
<211> 309  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1B with F46L mutation

<220>  
<221> CDS  
<222> (1)..(309)

<400> 230  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac 309  
Arg Thr Ile Phe Phe Lys Asp  
100

<210> 231  
<211> 103  
<212> PRT  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1B with F46L mutation

<400> 231

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15



Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile  
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp  
100

<210> 232  
<211> 306  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1B with F46L mutation and  
posit. 1 Met removed

<220>  
<221> CDS  
<222> (1)..(306)

<400> 232  
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144  
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys  
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
                     85                    90                    95

acc atc ttc ttc aag gac 306  
 Thr Ile Phe Phe Lys Asp  
                     100

<210> 233  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1B with F46L mutation and  
           posit. 1 Met removed

<400> 233

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1                    5                    10                    15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
                     20                    25                    30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys  
                     35                    40                    45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
                     50                    55                    60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65                    70                    75                    80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
                     85                    90                    95

Thr Ile Phe Phe Lys Asp  
                     100



<210> 234  
 <211> 309  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B with F64L mutation

<220>  
 <221> CDS  
 <222> (1)..(309)

<400> 234  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac 309  
 Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 235  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B with F64L mutation

<400> 235  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 236  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B with F64L mutation and posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 236  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

acc atc ttc ttc aag gac 306  
 Thr Ile Phe Phe Lys Asp

100

<210> 237  
<211> 102  
<212> PRT  
<213> Artificial

<220>

<223> modif. frag.; CFP F1B with F64L mutation and posit. 1 Met removed

<400> 237

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp  
100

<210> 238  
<211> 309  
<212> DNA  
<213> Artificial

<220>

<223> modif. frag.; CFP F1B with Y66W mutation

<220>

<221> CDS

<222> (1)..(309)

<400> 238

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20

25

30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
           35                          40                          45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
           50                          55                          60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
           65                          70                          75                          80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
                           85                          90                          95

cgc acc atc ttc ttc aag gac 309  
 Arg Thr Ile Phe Phe Lys Asp  
                           100

<210> 239  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B with Y66W mutation

<400> 239

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
   1                          5                          10                          15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
           20                          25                          30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
           35                          40                          45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
           50                          55                          60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
           65                          70                          75                          80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
                           85                          90                          95

Arg Thr Ile Phe Phe Lys Asp  
                           100

<210> 240  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B with Y66W mutation and posit. 1 Met removed  
 <220>  
 <221> CDS  
 <222> (1)..(306)

<400> 240  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac 306  
 Thr Ile Phe Phe Lys Asp  
 100

<210> 241  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B with Y66W mutation and posit. 1 Met removed

<400> 241

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp  
 100

<210> 242  
 <211> 309  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B with S65A mutation

<220>  
 <221> CDS  
 <222> (1)..(309)

<400> 242  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac 309  
 Arg Thr Ile Phe Phe Lys Asp

100

<210> 243  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B with S65A mutation

<400> 243

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 244  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B with S65A mutation and posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 244

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu



20

25

30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
           35                          40                          45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
           50                          55                          60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
           65                          70                          75                          80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
                           85                          90                          95

acc atc ttc ttc aag gac 306  
 Thr Ile Phe Phe Lys Asp  
                           100

<210> 245

<211> 102

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1B with S65A mutation and posit. 1 Met removed

<400> 245

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1                          5                          10                          15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
           20                          25                          30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
           35                          40                          45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
           50                          55                          60

Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
           65                          70                          75                          80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
                           85                          90                          95

Thr Ile Phe Phe Lys Asp  
                           100

<210> 246  
 <211> 309  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B, S65A, Y66W, and S72A mutations  
 <220>  
 <221> CDS  
 <222> (1)..(309)

<400> 246  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac 309  
 Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 247  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B, S65A, Y66W, and S72A mutations

<400> 247  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 248  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B, S65A,Y66W,and S72A mutations,  
 and posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 248  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

acc atc ttc ttc aag gac  
 Thr Ile Phe Phe Lys Asp  
 100

306

<210> 249  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B, S65A,Y66W,and S72A mutations,  
 and posit. 1 Met removed

<400> 249

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp  
 100

<210> 250  
 <211> 309  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B,F64L ,S65T, and Y66W mutations

<220>  
 <221> CDS  
 <222> (1)..(309)

<400> 250

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

48

1	5	10	15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc				96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly				
20		25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc				144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				
35		40	45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc				
192Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr				
50		55	60	
ctc acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag				240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys				
65		70	75	80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag				288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu				
85		90	95	
cgc acc atc ttc ttc aag gac				309
Arg Thr Ile Phe Phe Lys Asp				
100				

<210> 251  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1B,F64L ,S65T, and Y66W mutations

<400> 251

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20		25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35		40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50		55	60
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65		70	75
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85		90	95

Arg Thr Ile Phe Phe Lys Asp  
100

<210> 252  
<211> 306  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1B,F64L ,S65T, and Y66W mutations,  
and posit. 1 Met removed

<220>  
<221> CDS  
<222> (1)..(306)

<400> 252  
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15  
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30  
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45  
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
50 55 60  
acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80  
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95  
acc atc ttc ttc aag gac 306  
Thr Ile Phe Phe Lys Asp  
100

<210> 253  
<211> 102  
<212> PRT  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1B,F64L ,S65T, and Y66W mutations,  
and posit. 1 Met removed

<400> 253

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
50 55 60

Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp  
100

<210> 254

<211> 309

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1B, with Y66H mutation

<220>

<221> CDS

<222> (1)..(309)

<400> 254

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys



65		70		75		80										
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		

cgc	acc	atc	ttc	ttc	aag	gac	309
Arg	Thr	Ile	Phe	Phe	Lys	Asp	
			100				

<210> 255  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F1B, with Y66H mutation

<400> 255

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
		35					40					45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				

Phe	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70					75					80

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	

Arg	Thr	Ile	Phe	Phe	Lys	Asp
			100			

<210> 256  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F1B, with Y66H mutation and posit. 1  
 Met removed

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 256  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac 306  
 Thr Ile Phe Phe Lys Asp  
 100

<210> 257  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F1B, with Y66H mutation and posit. 1  
 Met removed

<400> 257  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp  
100

<210> 258  
<211> 309  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; BFP F1B, with F64L, Y66H mutations

<220>  
<221> CDS  
<222> (1)..(309)

<400> 258  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac 309  
Arg Thr Ile Phe Phe Lys Asp  
100

<210> 259  
 <211> 103  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F1B, with F64L, Y66H mutations  
 <400> 259

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp  
 100

<210> 260  
 <211> 306  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F1B, with F64L, Y66H mutations  
 and posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(306)

<400> 260  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60  
 ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac 306  
 Thr Ile Phe Phe Lys Asp  
 100

<210> 261  
 <211> 102  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F1B, with F64L, Y66H mutations  
 and posit. 1 Met removed

<400> 261

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60  
 Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 Thr Ile Phe Phe Lys Asp  
 100

<210> 262  
 <211> 411  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F2B (aa residues 104-240 of EYFP)  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(411)

<400> 262  
 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15  
 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30  
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45  
 gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80  
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95  
 aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110  
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125  
 act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 263  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F2B (aa residues 104-240 of EYFP)  
 and Met added @ posit. 1

<400> 263

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
35 40 45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 264

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; EGFP F2B(emerald), N146K, M153T, and I167T  
mutations

<220>

<221> CDS

<222> (1)..(408)

<400> 264

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly

	20	25	30	
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag gtc				144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val				
	35	40	45	
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag				192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys				
	50	55	60	
acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac				240
Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr				
	65	70	75	80
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac				288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn				
	85	90	95	
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag				336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys				
	100	105	110	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act				384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr				
	115	120	125	
ctc ggc atg gac gag ctg tac aag				408
Leu Gly Met Asp Glu Leu Tyr Lys				
	130	135		

<210> 265

<211> 136

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; EGFP F2B(emerald), N146K, M153T, and I167T mutations

<400> 265

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val
35 40 45

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
50 55 60

Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65 70 75 80





Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 266

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; EGFP F2B(emerald), N146K, M153T, and I167T  
mutations  
and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 266

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag 144  
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys  
35 40 45

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
50 55 60

aag acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336  
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
           115                          120                          125

act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
           130                          135

<210> 267  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; EGFP F2B(emerald), N146K, M153T, and I167T  
 mutations  
           and Met added @ posit. 1

<400> 267

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1                          5                          10                          15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
           20                          25                          30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys  
           35                          40                          45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
           50                          55                          60

Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65                          70                          75                          80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
           85                          90                          95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
           100                          105                          110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
           115                          120                          125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
           130                          135

<210> 268  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>

<223> modif. frag.; YFP F2B with Y203F mutation

<220>

<221> CDS

<222> (1)..(408)

<400> 268

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
1 5 10 15	

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
20 25 30	

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
35 40 45	

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
50 55 60	

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
65 70 75 80	

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
85 90 95	

cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
100 105 110	

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc act	384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
115 120 125	

ctc ggc atg gac gag ctg tac aag	408
Leu Gly Met Asp Glu Leu Tyr Lys	
130 135	

<210> 269  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>

<223> modif. frag.; YFP F2B with Y203F mutation

<400> 269

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
35 40 45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 270

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2B with Y203F mutation + Met @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 270

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac  
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

48

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac  
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

96

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
           35                                  40                                  45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
           50                                  55                                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
           65                                  70                                  75                                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
                                   85                                  90                                  95

aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
                                   100                                  105                                  110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
                                   115                                  120                                  125

act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
           130                                  135

<210> 271

<211> 137

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2B with Y203F mutation + Met @ posit. 1

<400> 271

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1                                  5                                  10                                  15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
                                   20                                  25                                  30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
           35                                  40                                  45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
           50                                  55                                  60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
           65                                  70                                  75                                  80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 272

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2B with Y203H mutation

<220>

<221> CDS

<222> (1)..(408)

<400> 272

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
35 40 45

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

115 120 125 408

ctc ggc atg gac gag ctg tac aag  
Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 273  
<211> 136  
<212> PRT  
<213> Artificial

<220>  
<223> modif. frag.; YFP F2B with Y203H mutation

<400> 273

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
35 40 45  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
50 55 60  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
65 70 75 80  
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95  
His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110  
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125  
Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 274  
<211> 411  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F2B with Y203H mutation +Met @ posit. 1



<220>  
 <221> CDS  
 <222> (1)..(411)

<400> 274  
 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15  
 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30  
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45  
 gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80  
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95  
 aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110  
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc 384  
 Lys Arg Asp His Met Val Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125  
 act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 275  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F2B with Y203H mutation + Met @ posit. 1

<400> 275  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95

Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 276

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2B with N146I mutation

<220>

<221> CDS

<222> (1)..(408)

<400> 276

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 35 40 45

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192  
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

65

70

75

80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
                     85                    90                    95

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
                     100                    105                    110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
                     115                    120                    125

ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
                     130                    135

<210> 277  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B with N146I mutation  
 <400> 277

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1                    5                    10                    15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
                     20                    25                    30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
                     35                    40                    45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
                     50                    55                    60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65                    70                    75                    80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
                     85                    90                    95

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
                     100                    105                    110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
                     115                    120                    125

Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 278  
 <211> 411  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B w. N146I mutation and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(411)

<400> 278  
 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15  
 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30  
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
 35 40 45  
 gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80  
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95  
 aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110  
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125  
 act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 279  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B w. N146I mutation and Met added @ posit. 1

<400> 279

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
 35 40 45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 280  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B with M153T mutation

<220>  
 <221> CDS  
 <222> (1)..(408)

<400> 280  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly

20						25						30						
aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	144		
Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val			
35						40						45						
tat	atc	act	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	192		
Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys			
50						55						60						
atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	240		
Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr			
65			70						75			80						
cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	288		
Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn			
			85						90			95						
cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	336		
His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys			
100						105						110						
cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	384		
Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr			
115						120						125						
ctc	ggc	atg	gac	gag	ctg	tac	aag									408		
Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys											
130						135												

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 282

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2B w. M153T mutation and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 282

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

ggc aac atc ctg ggc cac aag ctg gag tac aac tac aac agc cac aac 144  
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
35 40 45

gtc tat atc act gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
50 55 60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336  
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile



115

120

125

act ctc ggc atg gac gag ctg tac aag  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
       130                      135

411

<210> 283  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B w. M153T mutation and Met added @ posit. 1

<400> 283

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
   1                      5                      10                      15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
                       20                      25                      30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
                       35                      40                      45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
       50                      55                      60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
   65                      70                      75                      80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
                       85                      90                      95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
                       100                      105                      110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
                       115                      120                      125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
       130                      135

<210> 284  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B with N146I, M153T mutations

<220>  
 <221> CDS  
 <222> (1)..(408)

<400> 284  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30  
 aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 35 40 45  
 tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 50 55 60  
 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95  
 cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110  
 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125  
 ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 285  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B with N146I, M153T mutations

<400> 285

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 35 40 45

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 286  
 <211> 411  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B with N146I, M153T mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(411)

<400> 286  
 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15  
 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30  
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
 35 40 45  
 gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His

65

70

75

80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336  
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

act ctc ggc atg gac gag ctg tac aag 411  
Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 287  
<211> 137  
<212> PRT  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2B with N146I, M153T mutations  
and Met added @ posit. 1

<400> 287

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
35 40 45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 288  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B with V163A mutation

<220>  
 <221> CDS  
 <222> (1)..(408)

<400> 288  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 35 40 45  
 tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192  
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 50 55 60  
 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95  
 cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110  
 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125  
 ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 289  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>

<223> modif. frag.; CFP F2B with V163A mutation

<400> 289

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
35 40 45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 290

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2B w. V163A mutation and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 290

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp



20

25

30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45  
 gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192  
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80  
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95  
 aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110  
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125  
 act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 291  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B w. V163A mutation and Met added @ posit. 1  
 <400> 291

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45  
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
 50 55 60  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 292

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2B with N146I, V163A mutations

<220>

<221> CDS

<222> (1)..(408)

<400> 292

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
35 40 45

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

115                      120                      125  
 ctc ggc atg gac gag ctg tac aag  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130                      135

408

<210> 293  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B with N146I, V163A mutations

<400> 293

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1                      5                      10                      15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20                      25                      30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 35                      40                      45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 50                      55                      60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65                      70                      75                      80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85                      90                      95

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100                      105                      110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115                      120                      125

Leu Gly Met Asp Glu Leu Tyr Lys  
 130                      135

<210> 294  
 <211> 411  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B with N146I, V163A mutations

and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 294

atg	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	48
Met	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	
1				5					10					15		

acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	96
Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	
			20					25					30			

ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	atc	agc	cac	aac	144
Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser	His	Asn	
		35					40					45				

gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gcc	aac	ttc	192
Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Ala	Asn	Phe	
	50					55					60					

aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	240
Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	
65				70					75					80		

tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	288
Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	
				85					90					95		

aac	cac	tac	ctg	agc	act	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	336
Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	
			100					105					110			

aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	384
Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	
		115					120					125				

act	ctc	ggc	atg	gac	gag	ctg	tac	aag								411
Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys								
		130					135									

<210> 295

<211> 137

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2B with N146I, V163A mutations  
and Met added @ posit. 1

<400> 295

Met	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp
1				5					10					15	

Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	20		25		30
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn	35	40	45		
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe	50	55	60		
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His	65	70	75	80	
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp	85	90	95		
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu	100	105	110		
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile	115	120	125		
Thr Leu Gly Met Asp Glu Leu Tyr Lys	130	135			

<210> 296  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B with M153T, V163A mutations

<220>  
 <221> CDS  
 <222> (1)..(408)

<400> 296	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc	48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
1 5 10 15	
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc	96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
20 25 30	
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc	144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
35 40 45	
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
50 55 60	

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95

cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125

ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 297  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B with M153T, V163A mutations  
 <400> 297

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 35 40 45

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

115

120

125

Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

&lt;210&gt; 298

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

<223> modif. frag.; CFP F2B with M153T, V163A mutations  
and Met added @ posit. 1

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(411)

&lt;400&gt; 298

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

ggc aac atc ctg ggc cac aag ctg gag tac aac tac aac agc cac aac 144  
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
35 40 45

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192  
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
50 55 60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

aac cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag 336  
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

act ctc ggc atg gac gag ctg tac aag 411  
Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

&lt;210&gt; 299

&lt;211&gt; 137



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<212>  PRT
<213>  Artificial

<220>
<223>  modif. frag.; CFP F2B with M153T, V163A  mutations
        and Met added @ posit. 1

<400>  299

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1      5      10      15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
      20      25      30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
      35      40      45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
      50      55      60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65      70      75      80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
      85      90      95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
      100      105      110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
      115      120      125

Thr Leu Gly Met Asp Glu Leu Tyr Lys
      130      135

<210>  300
<211>  408
<212>  DNA
<213>  Artificial

<220>
<223>  modif. frag.; CFP F2B , N146I, M153T, and V163A mutations

<220>
<221>  CDS
<222>  (1)..(408)

<400>  300

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gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30  
 aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 35 40 45  
 tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 50 55 60  
 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95  
 cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110  
 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125  
 ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 301  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B , N146I, M153T, and V163A mutations

<400> 301

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 35 40 45

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys

50                      55                      60  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65                      70                      75                      80  
  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
                     85                      90                      95  
  
 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
                     100                      105                      110  
  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
                     115                      120                      125  
  
 Leu Gly Met Asp Glu Leu Tyr Lys  
                     130                      135

<210> 302  
 <211> 411  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B, N146I, M153T, and V163A mutations  
                     and Met added @ posit. 1  
  
 <220>  
 <221> CDS  
 <222> (1)..(411)

<400> 302  
 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac                      48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1                      5                      10                      15  
  
 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac                      96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
                     20                      25                      30  
  
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac                      144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
                     35                      40                      45  
  
 gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc                      192  
 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
                     50                      55                      60  
  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac                      240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65                      70                      75                      80  
  
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac                      288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
                     85                      90                      95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125

act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 303  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2B, N146I, M153T, and V163A mutations  
 and Met added @ posit. 1

<400> 303

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
 35 40 45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 304  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, w. N146I, T203Y mutations

<220>  
 <221> CDS  
 <222> (1)..(408)

<400> 304  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30  
 aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
 35 40 45  
 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192  
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 50 55 60  
 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95  
 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110  
 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125  
 ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 305  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, w. N146I, T203Y mutations

<400> 305

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
35 40 45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 306  
<211> 411  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CGFP F2B, w. N146I, T203Y mutations  
and Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(411)

<400> 306  
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15  
  
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30  
  
ggc aac atc ctg ggc cac aag ctg gag tac aac tac atc agc cac aac 144

Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser	His	Asn	
	35						40					45				
gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	192
Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	
	50					55				60						
aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	240
Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	
65					70				75						80	

tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	288
Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	
			85					90						95		

aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	336
Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	
			100					105						110		

aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	384
Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	
		115					120					125				

act	ctc	ggc	atg	gac	gag	ctg	tac	aag								411
Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys								
	130						135									

<210> 307  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, w. N146I, T203Y mutations  
 and Met added @ posit. 1

<400> 307

Met	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp
1			5						10					15	

Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp
			20					25					30		

Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser	His	Asn
		35					40					45			

Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe
	50					55					60				

Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His
65				70					75					80	

Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp
			85					90						95	

Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu
			100					105					110		

Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile
		115					120					125			



Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 308  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, w. M153T, T203Y mutations

<220>  
 <221> CDS  
 <222> (1)..(408)

<400> 308  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 35 40 45  
 tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 50 55 60  
 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95  
 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110  
 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125  
 ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 309  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>

<223> modif. frag.; CGFP F2B, w. M153T, T203Y mutations

<400> 309

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
35 40 45

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 310

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CGFP F2B, w. M153T, T203Y mutations  
and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 310

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45  
 gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80  
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95  
 aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110  
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125  
 act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 311  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, w. M153T, T203Y mutations  
 and Met added @ posit. 1

<400> 311

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 312

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CGFP F2B, N146I, M153T, and T203Y mutations

<220>

<221> CDS

<222> (1)..(408)

<400> 312

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
35 40 45

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192  
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
           115                          120                          125

ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
           130                          135

<210> 313  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, N146I, M153T, and T203Y mutations  
 <400> 313

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1                          5                          10                          15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
           20                          25                          30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
           35                          40                          45

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
           50                          55                          60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65                          70                          75                          80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
           85                          90                          95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
           100                          105                          110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
           115                          120                          125

Leu Gly Met Asp Glu Leu Tyr Lys  
           130                          135

<210> 314  
 <211> 411  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B,N146I, M153T, and T203Y mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(411)

<400> 314  
 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15  
 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30  
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
 35 40 45  
 gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80  
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95  
 aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110  
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125  
 act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 315  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B,N146I, M153T, and T203Y mutations  
 and Met added @ posit. 1

<400> 315

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp





tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag	192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
50 55 60	

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
65 70 75 80	

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
85 90 95	

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
100 105 110	

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
115 120 125	

ctc ggc atg gac gag ctg tac aag	408
Leu Gly Met Asp Glu Leu Tyr Lys	
130 135	

<210> 317

<211> 136

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CGFP F2B, w. V163A, T203Y mutations

<400> 317

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
35 40 45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
85 90 95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
---

100

105

110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 318

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CGFP F2B, w. V163A, T203Y mutations  
 and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 318

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192  
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
 50 55 60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125

act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 319  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, w. V163A, T203Y mutations  
 and Met added @ posit. 1

<400> 319

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 320  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B,N146I, V163A, and T203Y mutations

<220>  
 <221> CDS  
 <222> (1)..(408)

<400> 320  
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15  
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30  
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
35 40 45  
tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
50 55 60  
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
65 70 75 80  
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95  
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110  
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125  
ctc ggc atg gac gag ctg tac aag 408  
Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 321

<211> 136

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CGFP F2B,N146I, V163A, and T203Y mutations

<400> 321

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
35 40 45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 322  
 <211> 411  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, N146I,V163A, and T203Y mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(411)

<400> 322  
 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15  
 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30  
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
 35 40 45  
 gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192  
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

act ctc ggc atg gac gag ctg tac aag 411  
Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 323

<211> 137

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CGFP F2B, N146I,V163A, and T203Y mutations  
and Met added @ posit. 1

<400> 323

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
35 40 45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 324  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, M153T, V163A, and T203Y mutations

<220>  
 <221> CDS  
 <222> (1)..(408)

<400> 324  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 35 40 45  
 tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 50 55 60  
 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95  
 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110  
 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125  
 ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 325  
 <211> 136  
 <212> PRT  
 <213> Artificial



<220>  
 <223> modif. frag.; CGFP F2B, M153T, V163A, and T203Y mutations

<400> 325

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 35 40 45

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 326

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CGFP F2B, M153T, V163A, and T203Y mutations  
 and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 326

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15

48

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30  
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45  
 gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192  
 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80  
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95  
 aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110  
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125  
 act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 327  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, M153T, V163A, and T203Y mutations  
 and Met added @ posit. 1

<400> 327

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 328

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CGFP F2B, N146I, M153T, V163A, and T203Y mutations

<220>

<221> CDS

<222> (1)..(408)

<400> 328

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
35 40 45

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192  
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240  
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
                   100                                  105                                  110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
                   115                                  120                                  125

ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
                   130                                  135

<210> 329

<211> 136

<212> PRT<213> Artificial

<220>

<223> modif. frag.; CGFP F2B, N146I, M153T, V163A, and T203Y mutations

<400> 329

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1                                  5                                  10                                  15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
                   20                                  25                                  30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val  
                   35                                  40                                  45

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
                   50                                  55                                  60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 65                                  70                                  75                                  80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
                   85                                  90                                  95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
                   100                                  105                                  110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
                   115                                  120                                  125

Leu Gly Met Asp Glu Leu Tyr Lys  
                   130                                  135

<210> 330

<211> 411  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, N146I, M153T, V163A, and T203Y mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(411)

<400> 330  
 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15  
 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30  
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
 35 40 45  
 gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192  
 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65 70 75 80  
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95  
 aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110  
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125  
 act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 331  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2B, N146I, M153T, V163A, and T203Y mutations  
 and Met added @ posit. 1

<400> 331

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn  
35 40 45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 332

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F2B with Y145F mutation

<220>

<221> CDS

<222> (1)..(408)

<400> 332

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc	144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val	
35 40 45	
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag	192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
50 55 60	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac	240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
65 70 75 80	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
85 90 95	
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
100 105 110	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
115 120 125	
ctc ggc atg gac gag ctg tac aag	408
Leu Gly Met Asp Glu Leu Tyr Lys	
130 135	

<210> 333

<211> 136

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F2B with Y145F mutation

<400> 333

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
1 5 10 15	
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
20 25 30	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val	
35 40 45	
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys	
50 55 60	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr	
65 70 75 80	

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 334

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F2B w. Y145F mutation and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 334

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

ggc aac atc ctg ggc cac aag ctg gag tac aac ttc aac agc cac aac 144  
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn  
35 40 45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
50 55 60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240  
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336  
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc 384  
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile



115                                      120                                      125  
 act ctc ggc atg gac gag ctg tac aag                                      411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
     130                                      135  
  
 <210> 335  
 <211> 137  
 <212> PRT  
 <213> Artificial  
  
 <220>  
 <223> modif. frag.; BFP F2B w. Y145F mutation and Met added @ posit. 1  
  
 <400> 335  
  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1                                      5                                      10                                      15  
  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
                                     20                                      25                                      30  
  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn  
                                     35                                      40                                      45  
  
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
                                     50                                      55                                      60  
  
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
 65                                      70                                      75                                      80  
  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
                                     85                                      90                                      95  
  
 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
                                     100                                      105                                      110  
  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
                                     115                                      120                                      125  
  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
                                     130                                      135  
  
 <210> 336  
 <211> 408  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> modif. frag.; Venus F2B with S175G mutation

<220>  
 <221> CDS  
 <222> (1)..(408)  
  
 <400> 336  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15  
  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30  
  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 35 40 45  
  
 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192  
 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 50 55 60  
  
 atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 240  
 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
 65 70 75 80  
  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95  
  
 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110  
  
 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125  
  
 ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 337  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2B with S175G mutation

<400> 337  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15  
  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 35 40 45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 50 55 60

Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 338

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2B with S175G mutation and Met added @  
 posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 338

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192  
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
 50 55 60

aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac 240

Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His  
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
                     85                    90                    95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
                     100                    105                    110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
                     115                    120                    125

act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
                     130                    135

<210> 339  
 <211> 137  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2B with S175G mutation and Met added @  
 posit. 1

<400> 339

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1                    5                    10                    15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
                     20                    25                    30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
                     35                    40                    45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe  
                     50                    55                    60

Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His  
 65                    70                    75                    80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
                     85                    90                    95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
                     100                    105                    110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
                     115                    120                    125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 340  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2B w. M153T, S175G mutations

<220>  
 <221> CDS  
 <222> (1)..(408)

<400> 340  
 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15  
 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30  
 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144  
 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 35 40 45  
 tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192  
 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 50 55 60  
 atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 240  
 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
 65 70 75 80  
 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95  
 cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110  
 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125  
 ctc ggc atg gac gag ctg tac aag 408  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 341  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>

<223> modif. frag.; Venus F2B w. M153T, S175G mutations

<400> 341

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
35 40 45

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
50 55 60

Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 342

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2B w. M153T, S175G mutations  
and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 342

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96

Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp		
			20					25					30				
ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	144	
Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn		
		35					40				45						
gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	192	
Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe		
	50					55				60							
aag	atc	cgc	cac	aac	atc	gag	gac	ggc	ggc	gtg	cag	ctc	gcc	gac	cac	240	
Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Gly	Val	Gln	Leu	Ala	Asp	His		
65					70				75					80			
tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	288	
Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp		
			85					90					95				
aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	336	
Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu		
			100				105					110					
aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	384	
Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile		
		115				120					125						
act	ctc	ggc	atg	gac	gag	ctg	tac	aag								411	
Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys									
	130					135											

<210> 343

<211> 137

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2B w. M153T, S175G mutations  
and Met added @ posit. 1

<400> 343

Met	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp
1			5					10					15		

Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp
			20					25					30		

Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn
	35						40				45				

Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe
	50					55				60					

Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Gly	Val	Gln	Leu	Ala	Asp	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



65

70

75

80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 344

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2B w. V163A, S175G mutations

<220>

<221> CDS

<222> (1)..(408)

<400> 344

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48  
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96  
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144  
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
35 40 45

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192  
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
50 55 60

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 240  
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288  
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
85 90 95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336  
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384  
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

115 120 125 408

ctc ggc atg gac gag ctg tac aag  
 Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 345  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2B w. V163A, S175G mutations

<400> 345

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 35 40 45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys  
 50 55 60

Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr  
 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 85 90 95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 346  
 <211> 411  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2B w. V163A, S175G mutations

and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(411)

<400> 346

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144  
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
35 40 45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192  
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
50 55 60

aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac 240  
Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His  
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384  
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

act ctc ggc atg gac gag ctg tac aag 411  
Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 347

<211> 137

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2B w. V163A, S175G mutations  
and Met added @ posit. 1

<400> 347

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp

	20		25		30										
Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn
	35						40					45			
Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Ala	Asn	Phe
	50					55					60				
Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Gly	Val	Gln	Leu	Ala	Asp	His
	65				70					75				80	
Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp
				85					90					95	
Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu
			100					105						110	
Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile
		115					120					125			
Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys							
	130					135									

<210> 348  
 <211> 408  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2B, M153T, V163A, S175G mutations

<220>  
 <221> CDS  
 <222> (1)..(408)

<400>	348	
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc		48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr		
1 5 10 15		
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc		96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly		
20 25 30		
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc		144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val		
35 40 45		
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag		192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys		
50 55 60		

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac	240
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
65 70 75 80	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac	288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
85 90 95	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag	336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
100 105 110	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
115 120 125	
ctc ggc atg gac gag ctg tac aag	408
Leu Gly Met Asp Glu Leu Tyr Lys	
130 135	

<210> 349  
 <211> 136  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2B, M153T, V163A, S175G mutations  
 <400> 349

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr	
1 5 10 15	
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly	
20 25 30	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
35 40 45	
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys	
50 55 60	
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr	
65 70 75 80	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn	
85 90 95	
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys	
100 105 110	

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 350  
 <211> 411  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2B, M153T, V163A, S175G mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(411)

<400> 350  
 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48  
 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
 1 5 10 15  
 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96  
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
 20 25 30  
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144  
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
 35 40 45  
 gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192  
 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
 50 55 60  
 aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac 240  
 Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His  
 65 70 75 80  
 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288  
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
 85 90 95  
 aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336  
 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
 100 105 110  
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc 384  
 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 115 120 125  
 act ctc ggc atg gac gag ctg tac aag 411  
 Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 130 135

<210> 351  
 <211> 137  
 <212> PRT



<213> Artificial

<220>

<223> modif. frag.; Venus F2B, M153T, V163A, S175G mutations  
and Met added @ posit. 1

<400> 351

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
35 40 45

Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His  
65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
130 135

<210> 352

<211> 348

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1C (aa residues 1-117 of EYFP) with  
posit.1 Met removed

<220>

<221> CDS

<222> (1)..(348)

<400> 352

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val

48

1	5	10	15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag				96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu				
	20	25	30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc				144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys				
	35	40	45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc				192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe				
	50	55	60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg				240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg				
	65	70	75	80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc				288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg				
	85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg				336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val				
	100	105	110	
aag ttc gag ggc				348
Lys Phe Glu Gly				
	115			

<210> 353  
 <211> 116  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C (aa residues 1-117 of EYFP) with  
 posit.1 Met removed

<400> 353

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val				
1	5	10	15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu				
	20	25	30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys				
	35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe				
	50	55	60	
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg				
	65	70	75	80



His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 354  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1C, with F46L mutation

<220>  
<221> CDS  
<222> (1)..(351)

<400> 354  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 355

<211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C, with F46L mutation

<400> 355

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 356  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C w. F46L mutation & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 356

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

20								25								30								
ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ctg	atc	tgc	144								
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	Cys									
35						40						45												
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192								
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe									
50						55						60												
ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240								
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg									
65			70						75			80												
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288								
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg									
			85						90			95												
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336								
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val									
			100						105			110												
aag	ttc	gag	ggc													348								
Lys	Phe	Glu	Gly																					
115																								

<210> 357

<211> 116

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1C w. F46L mutation & posit. 1 Met removed

<400> 357

Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
1				5					10					15	

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
		20					25					30			

Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	Cys
		35					40					45			

Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe
	50					55					60				

Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg
65					70				75					80	

His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				85				90					95		

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 358  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1C with K79R mutation

<220>  
<221> CDS  
<222> (1)..(351)

<400> 358  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc 240  
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 359  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C with K79R mutation  
 <400> 359

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 360  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C w. K79R mutation & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 360  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

48



gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc	348
Lys Phe Glu Gly	
115	

<210> 361

<211> 116

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1C w. K79R mutation & posit. 1 Met removed

<400> 361

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 362  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1C with Y66F mutation

<220>  
<221> CDS  
<222> (1)..(351)

<400> 362  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 363

<211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C with Y66F mutation  
 <400> 363

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 364  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C w. Y66F mutation & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 364  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

20						25						30						
ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144		
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys			
35						40						45						
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192		
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe			
50						55						60						
ggc	ttc	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240		
Gly	Phe	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg			
65						70						75				80		
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288		
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg			
85						90						95						
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336		
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val			
100						105						110						
aag	ttc	gag	ggc													348		
Lys	Phe	Glu	Gly															
115																		

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 366  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1C with Q69K mutation

<220>  
<221> CDS  
<222> (1)..(351)

<400> 366  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 367  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C with Q69K mutation  
 <400> 367

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 368  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C w. Q69K mutation & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 368

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc	348
Lys Phe Glu Gly	
115	

<210> 369

<211> 116

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1C w. Q69K mutation & posit. 1 Met removed

<400> 369

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 370  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; citrine F1C w. V68L, Q69M mutations

<220>  
<221> CDS  
<222> (1)..(351)

<400> 370  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115



<210> 371  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine F1C w. V68L, Q69M mutations  
 <400> 371

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 372  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine F1C w. V68L, Q69M mutations  
 & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 372  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc	348
Lys Phe Glu Gly	
115	

<210> 373  
 <211> 116  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine F1C w. V68L, Q69M mutations  
 & posit. 1 Met removed

<400> 373

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 374  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1C w. F46L, F64L mutations

<220>  
<221> CDS  
<222> (1)..(351)

<400> 374  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 375  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C w. F46L, F64L mutations  
 <400> 375

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 376  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C w. F46L, F64L mutations  
 & posit.1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 376  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60  
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110  
 aag ttc gag ggc 348  
 Lys Phe Glu Gly  
 115

<210> 377  
 <211> 116  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1C w. F46L, F64L mutations  
 & posit.1 Met removed

<400> 377

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys  
 35 40 45  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 378  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1C w. F64L mutation

<220>  
<221> CDS  
<222> (1)..(351)

<400> 378  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ctc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 379  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1C w. F64L mutation  
 <400> 379

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 380  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.;CFP F1C w. F64L mutation & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 380

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc	348
Lys Phe Glu Gly	
115	

<210> 381

<211> 116

<212> PRT

<213> Artificial

<220>

<223> modif. frag.;CFP F1C w. F64L mutation & posit. 1 Met removed

<400> 381

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80



His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 382  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1C with Y66W mutation

<220>  
<221> CDS  
<222> (1)..(351)

<400> 382  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 383  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1C with Y66W mutation

<400> 383

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 384  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1C w. Y66W mutation & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 384

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc	348
Lys Phe Glu Gly	
115	

<210> 385

<211> 116

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP FlC w. Y66W mutation & posit. 1 Met removed

<400> 385

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 386  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1C with S65A mutation

<220>  
<221> CDS  
<222> (1)..(351)

<400> 386  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 387  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1C with S65A mutation  
 <400> 387

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 388  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1C w. S65A mutation & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 388  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc Lys Phe Glu Gly 115	348

<210> 389

<211> 116

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1C w. S65A mutation & posit. 1 Met removed

<400> 389

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15
--

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30
---

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45
---

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60
---

Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80
--

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 390  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1C ,S65A, Y66W, and S72A mutations

<220>  
<221> CDS  
<222> (1)..(351)

<400> 390  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 391  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1C ,S65A, Y66W, and S72A mutations  
 <400> 391

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 392  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1C , S65A, Y66W, and S72A mutations  
 & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 392  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val

48



1	5	10	15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag				96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu				
	20	25	30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc				144
Gly Glu Gly Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys				
	35	40	45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc				192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe				
	50	55	60	
gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg				240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg				
	65	70	75	80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc				288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg				
	85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg				336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val				
	100	105	110	
aag ttc gag ggc				348
Lys Phe Glu Gly				
	115			

<210> 393

<211> 116

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1C , S65A, Y66W, and S72A mutations  
& posit. 1 Met removed

<400> 393

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 394  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1C , F64L, S65T, and Y66W mutations

<220>  
<221> CDS  
<222> (1)..(351)

<400> 394  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 395  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1C , F64L, S65T, and Y66W mutations  
 <400> 395

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 396  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1C ,F64L, S65T, and Y66W mutations  
 & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 396  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

aag ttc gag ggc 348  
 Lys Phe Glu Gly  
 115

<210> 397  
 <211> 116  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1C ,F64L, S65T, and Y66W mutations  
 & posit. 1 Met removed

<400> 397

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60

Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 398  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; BFP F1C with Y66H mutation

<220>  
<221> CDS  
<222> (1)..(351)

<400> 398  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc 240  
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115

<210> 399  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F1C with Y66H mutation  
 <400> 399

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 400  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F1C w. Y66H mutation & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 400  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

48



His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 402  
<211> 351  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; BFP F1C w. F64L, Y66H mutations

<220>  
<221> CDS  
<222> (1)..(351)

<400> 402  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc 240  
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc 351  
Val Lys Phe Glu Gly  
115



<210> 403  
 <211> 117  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F1C w. F64L, Y66H mutations

<400> 403

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly  
 115

<210> 404  
 <211> 348  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F1C w. F64L, Y66H mutations  
 & posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(348)

<400> 404

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
50 55 60

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

aag ttc gag ggc 348  
Lys Phe Glu Gly  
115

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<220>
<223>  modif. frag.; BFP F1C w. F64L, Y66H mutations
      & posit. 1 Met removed
```

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly  
115

<210> 406  
<211> 369  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F2C and Met added @ position 1

<220>  
<221> CDS  
<222> (1)..(369)  
<223> YFP F2C corresponds to aa residues 118-239 of YFP

<400> 406  
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15  
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30  
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144  
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45  
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60  
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80  
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288  
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95  
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110  
ggg atc act ctc ggc atg gac gag ctg tac aag 369  
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 407  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F2C and Met added @ position 1

<400> 407

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 408  
 <211> 366  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F2C with Y203F mutation

<220>  
 <221> CDS  
 <222> (1)..(366)

<400> 408

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag  
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
 1 5 10 15

48

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac	96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
20 25 30	
aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac	144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
35 40 45	
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	
gac aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac	288
Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	
atc act ctc ggc atg gac gag ctg tac aag	366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
115 120	

<210> 409

<211> 122

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2C with Y203F mutation

<400> 409

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1 5 10 15

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
20 25 30

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
50 55 60

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65 70 75 80

Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 410  
<211> 369  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F2C w. Y203F mutation and Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(369)

<400> 410  
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15  
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30  
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144  
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45  
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60  
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80  
ccc gac aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc 288  
Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95  
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110  
ggg atc act ctc ggc atg gac gag ctg tac aag 369  
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 411  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F2C w. Y203F mutation and Met added @ posit. 1  
 <400> 411

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 412  
 <211> 366  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F2C with Y203H mutation

<220>  
 <221> CDS  
 <222> (1)..(366)

<400> 412  
 gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
 1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96  
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
 20 25 30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac 144  
 Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn  
 35 40 45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac 192  
 Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp  
 50 55 60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 240  
 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
 65 70 75 80

gac aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac 288  
 Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn  
 85 90 95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 336  
 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
 100 105 110

atc act ctc ggc atg gac gag ctg tac aag 366  
 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 413  
 <211> 122  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F2C with Y203H mutation

<400> 413

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
 1 5 10 15

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
 20 25 30

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn  
 35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp  
 50 55 60

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
 65 70 75 80



Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 414  
<211> 369  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F2C w. Y203H mutation and Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(369)

<400> 414  
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15  
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30  
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144  
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45  
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60  
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80  
ccc gac aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc 288  
Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95  
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110  
ggg atc act ctc ggc atg gac gag ctg tac aag 369  
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 415  
 <211> 123  
 <212> PRT  
 <213> Artificial  
  
 <220>  
 <223> modif. frag.; YFP F2C w. Y203H mutation and Met added @ posit. 1  
  
 <400> 415

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 416  
 <211> 366  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C with N146I mutation

<220>  
 <221> CDS  
 <222> (1)..(366)  
 <223> CFP F2C corresponds to residues 118-239 of YFP

<400> 416  
 gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
 1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac	96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
20 25 30	
aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac	144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
35 40 45	
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	
atc act ctc ggc atg gac gag ctg tac aag	366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
115 120	

<210> 417

<211> 122

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2C with N146I mutation

<400> 417

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
1 5 10 15	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
20 25 30	
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
35 40 45	
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 418  
<211> 369  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2C w. N146I mutation and Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(369)

<400> 418  
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15  
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 96  
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
20 25 30  
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144  
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45  
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60  
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80  
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288  
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95  
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110  
ggg atc act ctc ggc atg gac gag ctg tac aag 369  
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 419  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. N146I mutation and Met added @ posit. 1  
 <400> 419

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
 20 25 30

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 420  
 <211> 366  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C with M153T mutation

<220>  
 <221> CDS  
 <222> (1)..(366)  
 <400> 420

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag  
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
 1 5 10 15

48

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac	96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
20 25 30	
aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac	144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
35 40 45	
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	
atc act ctc ggc atg gac gag ctg tac aag	366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
115 120	

<210> 421  
 <211> 122  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C with M153T mutation

<400> 421

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1 5 10 15
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
20 25 30
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
35 40 45
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
50 55 60
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65 70 75 80

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 422  
<211> 369  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2C w. M153T mutation + Met @ posit. 1

<220>  
<221> CDS  
<222> (1)..(369)

<400> 422  
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15  
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30  
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144  
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45  
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60  
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80  
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288  
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95  
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110  
ggg atc act ctc ggc atg gac gag ctg tac aag 369  
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 423  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. M153T mutation and Met added @ posit. 1  
 <400> 423

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 424  
 <211> 366  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. N146I, M153T mutations

<220>  
 <221> CDS  
 <222> (1)..(366)

<400> 424  
 gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
 1 5 10 15



gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac 96  
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His  
 20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac 144  
 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn  
 35 40 45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac 192  
 Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp  
 50 55 60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 240  
 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
 65 70 75 80

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac 288  
 Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
 85 90 95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 336  
 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
 100 105 110

atc act ctc ggc atg gac gag ctg tac aag 366  
 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 425  
 <211> 122  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. N146I, M153T mutations

<400> 425

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
 1 5 10 15

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His  
 20 25 30

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn  
 35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp  
 50 55 60

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
 65 70 75 80

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 426  
<211> 369  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2C w. N146I, M153T mutations  
and Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(369)

<400> 426  
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15  
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 96  
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
20 25 30  
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144  
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45  
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60  
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80  
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288  
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95  
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110  
ggg atc act ctc ggc atg gac gag ctg tac aag 369  
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 427  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. N146I, M153T mutations  
 and Met added @ posit. 1

<400> 427

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
 20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 428  
 <211> 366  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C with V163A mutation

<220>  
 <221> CDS  
 <222> (1)..(366)

<400> 428

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag  
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
 1 5 10 15

48

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac	96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
20 25 30	
aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac	144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
35 40 45	
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	
atc act ctc ggc atg gac gag ctg tac aag	366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
115 120	

<210> 429  
 <211> 122  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C with V163A mutation  
 <400> 429

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
1 5 10 15	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
20 25 30	
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
35 40 45	
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 430  
<211> 369  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2C w. V163A mutation and Met added @ posit. 1

<220>  
<221> CDS  
<222> (1)..(369)

<400> 430  
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc 144  
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
35 40 45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288  
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

ggg atc act ctc ggc atg gac gag ctg tac aag 369  
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 431  
<211> 123

<212> PRT  
 <213> Artificial  
 <220>  
 <223> modif. frag.; CFP F2C w. V163A mutation and Met added @ posit. 1  
 <400> 431

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
 35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 432  
 <211> 366  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. N146I, V163A mutations  
 <220>  
 <221> CDS  
 <222> (1)..(366)

<400> 432  
 gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
 1 5 10 15  
 gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac 96  
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His  
 20 25 30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac	144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
35 40 45	

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	

atc act ctc ggc atg gac gag ctg tac aag	366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
115 120	

<210> 433  
 <211> 122  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. N146I, V163A mutations  
 <400> 433

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1 5 10 15

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
20 25 30

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
50 55 60

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65 70 75 80

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110



Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 434  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. N146I, V163A mutations and  
 Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 434  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
 20 25 30  
 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc 144  
 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 435  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. N146I, V163A mutations and  
 Met added @ posit. 1

<400> 435

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
20 25 30

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 436

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2C w. M153T, V163A mutations

<220>

<221> CDS

<222> (1)..(366)

<400> 436

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac 144  
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn  
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac	288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	
atc act ctc ggc atg gac gag ctg tac aag	366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
115 120	

<210> 437  
 <211> 122  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. M153T, V163A mutations

<400> 437

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
1 5 10 15	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
20 25 30	
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
35 40 45	
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 438  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. M153T, V163A mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 438  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30  
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc 144  
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 439  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C w. M153T, V163A mutations  
 and Met added @ posit. 1

<400> 439

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 440

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2C, N146I, M153T, and V163A mutations

<220>

<221> CDS

<222> (1)..(366)

<400> 440

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His  
20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac 144  
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn  
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac 192  
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp  
50 55 60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 240  
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
65 70 75 80

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac 288  
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 336  
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

atc act ctc ggc atg gac gag ctg tac aag 366  
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 441  
<211> 122  
<212> PRT  
<213> Artificial

<220>  
<223> modif. frag.; CFP F2C, N146I, M153T, and V163A mutations  
<400> 441

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His  
20 25 30

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn  
35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp  
50 55 60

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
65 70 75 80

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 442  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C, N146I, M153T, and V163A mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)...(369)

<400> 442  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
 20 25 30  
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc 144  
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 443  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F2C, N146I, M153T, and V163A mutations

and Met added @ posit. 1

<400> 443

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 444

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CGFP F2C w. M153T, T203Y mutations

<220>

<221> CDS

<222> (1)..(366)

<223> CGFP F2C corresponds to residues 118-239 of YFP

<400> 444

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac 144



Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn		
	35						40					45					
ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	192	
Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp		
	50					55					60						
cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	240	
His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro		
	65				70					75					80		
gac	aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	288	
Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn		
				85				90					95				
gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	336	
Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly		
			100					105					110				
atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag							366	
Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys								
		115					120										
<210>	445																
<211>	122																
<212>	PRT																
<213>	Artificial																
<220>																	
<223>	modif. frag.; CGFP F2C w. M153T, T203Y mutations																
<400>	445																
Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu		
1				5					10					15			
Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His		
		20						25					30				
Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn		
	35						40					45					
Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp		
	50					55					60						
His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro		
	65				70				75						80		
Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn		
				85					90					95			
Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly		
			100					105					110				



Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 446  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C w. M153T, T203Y mutations and  
 Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 446  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30  
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144  
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 447  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C w. M153T, T203Y mutations and  
 Met added @ posit. 1

<400> 447

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 448

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CGFP F2C w. V163A, T203Y mutations

<220>

<221> CDS

<222> (1)..(366)

<400> 448

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac 144  
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn  
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	
gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac	288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	
atc act ctc ggc atg gac gag ctg tac aag	366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
115 120	

<210> 449  
 <211> 122  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C w. V163A, T203Y mutations

<400> 449

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
1 5 10 15	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
20 25 30	
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
35 40 45	
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 450  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C w. V163A, T203Y mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 450  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30  
 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc 144  
 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 451  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C w. V163A, T203Y mutations  
 and Met added @ posit. 1

<400> 451

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 452

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CGFP F2C, N146I, M153T, and T203Y mutations

<220>

<221> CDS

<222> (1)..(366)

<400> 452

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His  
20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac 144  
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn  
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac	288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	

atc act ctc ggc atg gac gag ctg tac aag	366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
115 120	

<210> 453

<211> 122

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CGFP F2C, N146I, M153T, and T203Y mutations

<400> 453

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1 5 10 15

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
20 25 30

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
50 55 60

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65 70 75 80

Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
100 105 110



Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 454  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C, N146I, M153T, and T203Y mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 454  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
 20 25 30  
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144  
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 455  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C, N146I, M153T, and T203Y mutations

and Met added @ posit. 1

<400> 455

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 456

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CGFP F2C, M153T, V163A, and T203Y mutations

<220>

<221> CDS

<222> (1)..(366)

<400> 456

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac 144  
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn

35	40	45	
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac			192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp			
50	55	60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc			240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro			
65	70	75	80
gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac			288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn			
	85	90	95
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg			336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly			
	100	105	110
atc act ctc ggc atg gac gag ctg tac aag			366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			
	115	120	

<210> 457

<211> 122

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CGFP F2C, M153T, V163A, and T203Y mutations

<400> 457

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1 5 10 15

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
20 25 30

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
50 55 60

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65 70 75 80

Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
100 105 110

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 458  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C, M153T, V163A, and T203Y mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 458  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30  
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc 144  
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 459  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C, M153T, V163A, and T203Y mutations

and Met added @ posit. 1

<400> 459

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 460

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CGFP F2C, N146I, M153T, V163A, and T203Y mutations

<220>

<221> CDS

<222> (1)..(366)

<400> 460

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His  
20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac 144  
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn  
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac	192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc	240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	
gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac	288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg	336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	
atc act ctc ggc atg gac gag ctg tac aag	366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
115 120	

<210> 461  
 <211> 122  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C, N146I, M153T, V163A, and T203Y mutations

<400> 461

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
1 5 10 15	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
20 25 30	
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	
35 40 45	
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
50 55 60	
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	
65 70 75 80	
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn	
85 90 95	
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly	
100 105 110	

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 462  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C, N146I, M153T, V163A, and T203Y mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 462  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
 20 25 30  
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc 144  
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 463  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CGFP F2C, N146I, M153T, V163A, and T203Y mutations  
 and Met added @ posit. 1



<400> 463

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 464

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F2C w. Y145F mutation

<220>

<221> CDS

<222> (1)..(366)

<223> BFP F2C corresponds to aa residues 118-239 of YFP

<400> 464

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His  
20 25 30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac 144  
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn

35	40	45	
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac			192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp			
50	55	60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc			240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro			
65	70	75	80
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac			288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn			
85	90	95	
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg			336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly			
100	105	110	
atc act ctc ggc atg gac gag ctg tac aag			366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			
115	120		
<210> 465			
<211> 122			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; BFP F2C w. Y145F mutation			
<400> 465			
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu			
1	5	10	15
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His			
20	25	30	
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn			
35	40	45	
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp			
50	55	60	
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro			
65	70	75	80
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn			
85	90	95	
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly			
100	105	110	

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 466  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F2C w. Y145F mutation and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 466  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser  
 20 25 30  
 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144  
 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 467  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; BFP F2C w. Y145F mutation and Met added @ posit. 1

<400> 467

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser  
20 25 30

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 468

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2C with S175G mutation

<220>

<221> CDS

<222> (1)..(366)

<223> Venus F2C corresponds to aa residues 118-239 of YFP

<400> 468

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac 144  
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn

35	40	45	
ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac			192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp			
50	55	60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc			240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro			
65	70	75	80
gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac			288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn			
85	90	95	
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg			336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly			
100	105	110	
atc act ctc ggc atg gac gag ctg tac aag			366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			
115	120		

<210> 469  
 <211> 122  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2C with S175G mutation  
 <400> 469

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu			
1	5	10	15
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His			
20	25	30	
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn			
35	40	45	
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp			
50	55	60	
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro			
65	70	75	80
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn			
85	90	95	
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly			
100	105	110	

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 470  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2C w. S175G mutation + Met @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 470  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30  
 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144  
 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 471  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2C w. S175G mutation + Met @ posit. 1

<400> 471

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 472

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2C w. M153T, S175G mutations

<220>

<221> CDS

<222> (1)..(366)

<400> 472

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac 144  
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn  
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac 192  
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp  
50 55 60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 240  
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
65 70 75 80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac 288  
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 336  
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

atc act ctc ggc atg gac gag ctg tac aag 366  
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 473  
<211> 122  
<212> PRT  
<213> Artificial

<220>  
<223> modif. frag.; Venus F2C w. M153T, S175G mutations

<400> 473

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn  
35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp  
50 55 60

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
65 70 75 80

Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110



Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 474  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2C w. M153T, S175G mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 474  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30  
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144  
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 475  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2C w. M153T, S175G mutations  
 and Met added @ posit. 1

<400> 475

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 476

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2C w. V163A, S175G mutations

<220>

<221> CDS

<222> (1)..(366)

<400> 476

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac 144  
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn  
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac 192  
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp  
50 55 60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 240  
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
65 70 75 80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac 288  
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 336  
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

atc act ctc ggc atg gac gag ctg tac aag 366  
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 477  
<211> 122  
<212> PRT  
<213> Artificial

<220>  
<223> modif. frag.; Venus F2C w. V163A, S175G mutations  
<400> 477

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn  
35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp  
50 55 60

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
65 70 75 80

Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 478  
 <211> 369  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2C w. V163A, S175G mutations  
 and Met added @ posit. 1

<220>  
 <221> CDS  
 <222> (1)..(369)

<400> 478  
 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48  
 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 1 5 10 15  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
 20 25 30  
 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc 144  
 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
 35 40 45  
 aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc 192  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala  
 50 55 60  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 65 70 75 80  
 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288  
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
 85 90 95  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 100 105 110  
 ggg atc act ctc ggc atg gac gag ctg tac aag 369  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 479  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; Venus F2C w. V163A, S175G mutations  
 and Met added @ posit. 1

<400> 479

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 480

<211> 366

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2C, M153T, V163A, and S175G mutations

<220>

<221> CDS

<222> (1)..(366)

<400> 480

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac 144  
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn  
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac 192  
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp  
50 55 60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 240  
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
65 70 75 80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac 288  
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 336  
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

atc act ctc ggc atg gac gag ctg tac aag 366  
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 481

<211> 122

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2C, M153T, V163A, and S175G mutations

<400> 481

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
1. 5 10 15

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
20 25 30

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn  
35 40 45

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp  
50 55 60

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
65 70 75 80

Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
85 90 95

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
100 105 110

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 115 120

<210> 482

<211> 369

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2C, M153T, V163A, and S175G mutations  
 and Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(369)

<400> 482

atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag	48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	
1 5 10 15	

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc	96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser	
20 25 30	

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc	144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala	
35 40 45	

aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc	192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala	
50 55 60	

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg	240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	
65 70 75 80	

ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc	288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro	
85 90 95	

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc	336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	
100 105 110	

ggg atc act ctc ggc atg gac gag ctg tac aag	369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
115 120	

<210> 483

<211> 123

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2C, M153T, V163A, and S175G mutations

and Met added @ posit. 1

<400> 483

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala  
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro  
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
115 120

<210> 484

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1DX w. position 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<223> YFP F1DX fragment corresponds to aa residues 1-158 of YFP

<400> 484

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144



Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
		35					40					45					
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192	
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		
	50					55					60						
ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240	
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		
65				70					75					80			
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288	
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
				85				90						95			
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336	
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
			100					105					110				
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384	
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
		115					120					125					
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432	
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
	130					135					140						
tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag				471	
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln					
145					150					155							

<210> 485  
 <211> 157  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1DX w. position 1 Met removed  
 <400> 485

Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1				5					10					15			
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
		20						25					30				
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
		35					40					45					
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		
	50					55					60						
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		
65				70					75					80			



His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
145 150 155

<210> 486  
<211> 474  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1DX with K79R mutation

<220>  
<221> CDS  
<222> (1)..(474)

<400> 486  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtg aag ttc gag ggc gac acc ctg	gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu	Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125	
atc gac ttc aag gag gac ggc aac atc	ctg ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile	Leu Gly His Lys Leu Glu Tyr		
130	135	140	
aac tac aac agc cac aac gtc tat atc	atg gcc gac aag cag		474
Asn Tyr Asn Ser His Asn Val Tyr Ile	Met Ala Asp Lys Gln		
145	150	155	

<210> 487

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1DX with K79R mutation

<400> 487

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 488  
 <211> 471  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1DX, w. K79R mutation, and posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(471)

<400> 488  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110  
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125  
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140  
 tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471  
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 489  
<211> 157  
<212> PRT  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1DX, w. K79R mutation, and posit. 1 Met removed

<400> 489

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
145 150 155

<210> 490  
<211> 474  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1DX with Y66F mutation

<220>  
 <221> CDS  
 <222> (1)..(474)

<400> 490

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55				60						
ttc	ggc	ttc	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Gly	Phe	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75					80		
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85				90						95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag			474
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln			
145					150				155							

<210> 491  
 <211> 158  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1DX with Y66F mutation

<400> 491

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 492  
 <211> 471  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1DX, Y66F mutation, and posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(471)

<400> 492  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45



acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
145 150 155	

<210> 493

<211> 157

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1DX, Y66F mutation, and posit. 1 Met removed

<400> 493

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
145 150 155

<210> 494  
<211> 474  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; YFP F1DX with Q69K mutation

<220>  
<221> CDS  
<222> (1)..(474)

<400> 494  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

	100		105		110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc						384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly						
	115		120		125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac						432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr						
	130		135		140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag						474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln						
	145		150		155	

<210> 495

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1DX with Q69K mutation

<400> 495

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 496  
 <211> 471  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1DX, Q69K mutation, and posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(471)

<400> 496  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110  
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125  
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140  
 tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471  
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 497

<211> 157  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; YFP F1DX, Q69K mutation, and posit. 1 Met removed  
 <400> 497

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 498  
 <211> 474  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine F1DX with V68L, Q69M mutations

<220>  
 <221> CDS  
 <222> (1)..(474)

<400> 498

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					

ttc	ggc	tac	ggc	ctg	atg	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Gly	Tyr	Gly	Leu	Met	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75						80	

cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		

cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			

gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				

atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					

aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag			474
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln			
145					150					155						

<210> 499  
 <211> 158  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine F1DX with V68L, Q69M mutations

<400> 499

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5				10					15		

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 500  
 <211> 471  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine F1DX, V68L and Q69M mutations,  
 and position 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(471)

<400> 500  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110  
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125  
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140  
 tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471  
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 501  
 <211> 157  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; citrine F1DX, V68L and Q69M mutations,  
 and position 1 Met removed

<400> 501

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60



Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
145 150 155

<210> 502  
<211> 474  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1DX with F64L mutation

<220>  
<221> CDS  
<222> (1)..(474)

<400> 502  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

	85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag				336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				
	100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc				384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				
	115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac				432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				
	130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag				474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln				
	145	150	155	

<210> 503

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX with F64L mutation

<400> 503

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
		35					40					45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				

Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70					75					80

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105					110		

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 504

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX w. F64L mutation, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 504

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471  
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln

145

150

155

<210> 505  
 <211> 157  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. F64L mutation, and posit. 1 Met removed  
 <400> 505

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 506  
 <211> 474  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX, F64L, S65T, and Y66W mutations  
 <220>

<221> CDS  
 <222> (1)..(474)

<400> 506

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ctg	acc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75						80	
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130				135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag			474
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln			
145					150					155						

<210> 507

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, F64L, S65T, and Y66W mutations

<400> 507

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 508  
 <211> 471  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX, F64L, S65T, and Y66W mutations,  
 and position 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(471)

<400> 508  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144

Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
		50				55					60					
acc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Thr	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65					70					75					80	
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95		
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
				100				105					110			
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130				135					140					
tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag				471
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln				
145					150					155						
<210> 509																
<211> 157																
<212> PRT																
<213> Artificial																
<220>																
<223> modif. frag.; CFP F1DX, F64L, S65T, and Y66W mutations, and position 1 Met removed																
<400> 509																
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1				5					10					15		
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			20					25					30			
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
		50				55					60					
Thr	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	



65

70

75

80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
145 150 155

<210> 510  
<211> 474  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1DX with Y66W mutation

<220>  
<221> CDS  
<222> (1)..(474)

<400> 510  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtg aag ttc gag ggc gac acc ctg	gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu	Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag			474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln			
145	150	155	

<210> 511  
 <211> 158  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX with Y66W mutation

<400> 511

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 512  
 <211> 471  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. Y66W mutation, and posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(471)

<400> 512  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110  
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125  
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140  
 tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471  
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 513  
 <211> 157  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. Y66W mutation, and posit. 1 Met removed  
 <400> 513

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 514  
 <211> 474  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. Y66W, N146I mutations  
 <220>

<221> CDS  
 <222> (1)..(471)  
  
 <400> 514  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
  
 ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
  
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
  
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
  
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
  
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
  
 aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag 474  
 Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys  
 145 150 155  
  
 <210> 515  
 <211> 157  
 <212> PRT  
 <213> Artificial  
  
 <220>  
 <223> modif. frag.; CFP F1DX w. Y66W, N146I mutations  
  
 <400> 515  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20	25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35	40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50	55	60
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys		
65	70	75
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys		
145	150	155

<210> 516  
 <211> 471  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. Y66W, N146I mutations, and  
 posit. 1 Met removed

<220>  
 <221> CDS  
 <222> (1)..(471)

<400> 516		
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc		48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1	5	10
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag		96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20	25	30
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc		144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
35	40	45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac atc agc cac aac gtc tat atc atg gcc gac aag cag	471
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
145 150 155	

<210> 517  
 <211> 157  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. Y66W, N146I mutations, and  
 posit. 1 Met removed

<400> 517

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	



His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
145 150 155

<210> 518  
<211> 474  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1DX w. Y66W, M153T mutations

<220>  
<221> CDS  
<222> (1)..(474)

<400> 518  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtg aag ttc gag ggc gac acc ctg	gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr	Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag			474
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln			
145	150	155	
 <210> 519			
<211> 158			
<212> PRT			
<213> Artificial			
 <220>			
<223> modif. frag.; CFP F1DX w. Y66W, M153T mutations			
 <400> 519			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
 145 150 155

<210> 520

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX w. Y66W, M153T mutations, and  
 posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 520

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
 ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
 tac aac agc cac aac gtc tat atc acc gcc gac aag cag	471
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	
145 150 155	

<210> 521  
 <211> 157  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. Y66W, M153T mutations, and  
 posit. 1 Met removed

<400> 521

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
 145 150 155

<210> 522  
 <211> 474  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX with N146I mutation

<220>  
 <221> CDS  
 <222> (1)..(474)

<400> 522  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag 474  
 Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 523  
 <211> 158  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX with N146I mutation

<400> 523

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
145 150 155

<210> 524

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX w. N146I mutation, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 524

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35

40

45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110  
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125  
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140  
 tac atc agc cac aac gtc tat atc atg gcc gac aag cag 471  
 Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 145 150 155

<210> 525  
 <211> 157  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. N146I mutation, and posit. 1 Met removed

<400> 525

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80



His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
145 150 155

<210> 526  
<211> 474  
<212> DNA  
<213> Artificial

<220>  
<223> modif. frag.; CFP F1DX with M153T mutation

<220>  
<221> CDS  
<222> (1)..(474)

<400> 526  
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu



Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
 145 150 155

<210> 528  
 <211> 471  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. M153T mutation, and posit. 1  
 Met removed

<220>  
 <221> CDS  
 <222> (1)..(471)

<400> 528  
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15  
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30  
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45  
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60  
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80  
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95  
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110  
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125  
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140  
 tac aac agc cac aac gtc tat atc acc gcc gac aag cag 471  
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
 145 150 155

<210> 529  
 <211> 157  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. M153T mutation, and posit. 1  
 Met removed

<400> 529

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
 145 150 155

<210> 530  
 <211> 474  
 <212> DNA  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. N146I, M153T mutations

<220>  
 <221> CDS  
 <222> (1)..(474)

<400> 530  
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag 474  
 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
 145 150 155

<210> 531  
 <211> 158  
 <212> PRT  
 <213> Artificial

<220>  
 <223> modif. frag.; CFP F1DX w. N146I, M153T mutations

<400> 531  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
 145 150 155

<210> 532

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, N146I, M153T mutations, and posit. 1  
 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 532

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35

40

45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192  
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240  
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432  
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag 471  
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
145 150 155

<210> 533

<211> 157

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, N146I, M153T mutations, and posit. 1  
Met removed

<400> 533

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg  
65 70 75 80



His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
145 150 155

<210> 534

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, Y66W, N146I, and M153T mutations

<220>

<221> CDS

<222> (1)..(474)

<400> 534

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336